

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 15:11:39 ; Search time 2585.24 Seconds
(without alignments)
9747.064 Million cell updates/sec

Title: US-09-788-074-4
Perfect score: 662
Sequence: 1 accgcgcagcagaccctc.....taataaatgtgttctgtcct 662

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	658.4	99.5	692	4	BM670233 UI-E-DW1-
2	657	99.2	712	5	BU533478 AGENCOURT
3	655.4	99.0	662	5	BX385751 BX385751
4	655.2	99.0	717	4	BG719235 602690296
5	650.8	98.3	820	4	BG678687 602624485
6	647	97.7	788	1	AV727829 AV727829
7	644.2	97.3	706	4	BG715536 602675842
8	643.8	97.3	748	5	BU943612 AGENCOURT
9	643	97.1	666	4	BM789868 K-EST0069
10	640.8	96.8	843	5	BU601920 AGENCOURT
11	640.4	96.7	656	1	AV724494 AV724494
12	639.4	96.6	686	6	CB530038 UI-H-FT2-
13	636	96.1	655	5	BQ446473 UI-H-EUI-
14	632.8	95.6	654	6	CD370550 UI-H-FT1-
15	632.4	95.5	799	5	BU532649 AGENCOURT
16	632.2	95.5	668	1	AV726696 AV726696
17	631.4	95.4	664	4	BG179048 602330759
18	628.2	94.9	873	5	BU941286 AGENCOURT
19	627	94.7	631	5	BX404021 BX404021
20	626.8	94.7	644	4	AI080481 0871d05.x
21	625	94.4	668	4	BG168846 602320168
22	624.8	94.4	769	5	BU955447 AGENCOURT
23	624.4	94.3	684	4	BF981201 602310488
24	620	93.7	642	5	BU783805 in09g12.x

25	620	93.7	664	2	BF341608	BF341608 602016030
26	619.6	93.6	761	5	BU963854	BU963854 AGENCOURT
C 27	618.8	93.5	654	4	BM665113	BM665113 UI-E-CQ1-
28	618	93.4	632	6	CB124107	CB124107 K-EST0172
29	615.6	93.0	781	5	BU953727	BU953727 AGENCOURT
30	615.4	93.0	629	4	BM695640	BM695640 UI-E-CQ1-
31	614	92.7	625	4	BM695742	BM695742 UI-E-CQ1-
32	613.4	92.7	615	6	CD679571	CD679571 hq13b11.y
33	612.8	92.6	653	4	BM459183	BM459183 AGENCOURT
34	611	92.3	634	6	CD677981	CD677981 ho25c09.y
C 35	610	92.1	646	4	BM666524	BM666524 UI-E-CQ1-
C 36	608.6	91.9	644	1	AI857611	AI857611 wk95d09.x
37	606	91.5	632	4	BM791091	BM791091 K-EST0071
38	605	91.4	653	2	BF035373	BF035373 601458587
39	603.2	91.1	678	7	CN644162	CN644162 ILLUMIGEN
C 40	602.8	91.1	659	1	AI338767	AI338767 qt53d02.x
41	601.6	90.9	666	5	BX338755	BX338755 BX338755
42	600	90.6	747	5	BU955273	BU955273 AGENCOURT
43	598.4	90.4	614	6	CB138668	CB138668 K-EST0191
C 44	598.2	90.4	654	2	AW009545	AW009545 w884d08.x
45	597.6	90.3	653	6	CD389254	CD389254 AGENCOURT

ALIGNMENTS

RESULT 1
BM670233/c
LOCUS BM670233 692 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-DW1-ahc-h-08-0-UI.e1 UI-E-DW1 Homo sapiens cDNA clone
UI-E-DW1-ahc-h-08-0-UI 3', mRNA sequence.
ACCESSION BM670233
VERSION BM670233.1 GI:18980130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 692)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PubMed 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=yes.
Location/Qualifiers
1. .692
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-DW1-ahc-h-08-0-UI"
/tissue_type="adult"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-DW1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-DW1 is a normalized cDNA library containing the

FEATURES
source

following tissue(s): lens. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p7773-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG TISSUE=human lens
TAG_LIB=UI-E-DW1
TAG_SEQ=CGATTAGCGA "

ORIGIN

```

Query Match          99.5%; Score 658.4; DB 4; Length 692;
Best Local Similarity 99.8%; Pred. No. 3.3e-149;
Matches 659; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3  CGCCGACGAGACCCCTCTCTGCACGCCAGCCCGCCGCCACCCACCATGGCCACAGTTCA 62
Db 678 CGCCGACGAGACCCCTCTCTGCACGCCAGCCCGCCGCCACCCACCATGGCCACAGTTCA 619

QY 63  GCAGCTGGAGGAAGATGCGCGCTGGTGACAGCAAGAGCTTTGATGATACATGAAGGA 122
Db 618 GCAGCTGGAGGAAGATGCGCGCTGGTGACAGCAAGAGCTTTGATGATACATGAAGGA 559

QY 123 GCTAGAGTGGGAATAGCTTTTCGAAAATATGGGCGCAATGGCCAGCCAGATTGTATCAT 182
Db 558 GCTAGAGTGGGAATAGCTTTTCGAAAATATGGGCGCAATGGCCAGCCAGATTGTATCAT 499

QY 193 CACTTGTGATGTATAAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGTT 242
Db 498 CACTTGTGATGTATAAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGTT 439

QY 243 TTCCTGTACCTCGGAGAGAGTTTGAAGAACCAACAGCTGATGCGAAGAACTCAGAC 302
Db 438 TTCCTGTACCTCGGAGAGAGTTTGAAGAACCAACAGCTGATGCGAAGAACTCAGAC 379

QY 303 TGCTGCAACTTTACAGATGGTGCAATGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 362
Db 378 TGCTGCAACTTTACAGATGGTGCAATGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 319

QY 363 CACAATAACAAGAAATGAAGATGGGAAATAGTGGTGGAGTGTGTATGAAACAATGT 422
Db 318 CACAATAACAAGAAATGAAGATGGGAAATAGTGGTGGAGTGTGTATGAAACAATGT 259

QY 423 CACCTGTACTCGGATCTATGAAAAGTAGAATAAAATTCATCATCTTGGACAGGA 482
Db 258 CACCTGTACTCGGATCTATGAAAAGTAGAATAAAATTCATCATCTTGGACAGGA 199

QY 483 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATAGCAAACTCCATCTACTGTTCTTCT 542
Db 198 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATAGCAAACTCCATCTACTGTTCTTCT 139

QY 543 TTTTCTTTTCACTACTGTGTTCAATTAATCTTTATCATAAACATTTTATCATGCACTATT 602
Db 138 TTTTCTTTTCACTACTGTGTTCAATTAATCTTTATCATAAACATTTTATCATGCACTATT 79

QY 603 CAAAGTGTGGATTAATTAGATCATCCCTTTGGTTAATAAATAATGTTGTGCT 662
Db 78 CAAAGTGTGGATTAATTAGATCATCCCTTTGGTTAATAAATAATGTTGTGCT 19
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RESULT 2

BU533478
 LOCUS 712 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGENCOURT_10197890 NIH_MGC_126 Homo sapiens cDNA clone
 IMAGE:6559866 5', mRNA sequence.
 ACCESSION BU533478
 VERSION BU533478.1 GI:22843919

KEYWORDS

SOURCE ORGANISM

EST. Homo sapiens (human)

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (Bases 1 to 712)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

AUTHORS

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L10M2731 row: m column: 18

High quality sequence stop: 630.

FEATURES

source

1..712

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6559866"

/tissue_type="mixed (pool of 40 RNAs)"

/lab_host="DH10B (TI-phage-resistant)"

/clone_lib="NIH_MGC_126"

/note="Vector: pBMR-LiB; Site 1: SfiI (ggccattatggcc);

Site 2: SfiI (ggcgccctcgcc); Double-stranded cDNA was

prepared from a pool of 40 cell line polyA+ RNAs (bladder

2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,

kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -

5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,

salivary gland - 1.3%, and skin - 2.3%). 5' and 3'

adaptors were used in cloning as follows:

5'-RAGCAGTGTATCAGCAGAGTGGCATACGGCGGG-3' and

5'-ATTCTAGAGCGCGGCGCGGCACATG-dT(30)NN-3'. Full-length

enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.5-1

kb size fraction (other fractions present in NIH_MGC_127

and NIH_MGC_128). Library created in the laboratory of T.

Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC

ORIGIN

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Query Match          99.2%; Score 657; DB 5; Length 712;
Best Local Similarity 100.0%; Pred. No. 7.3e-149;
Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3  CGCCGACGAGACCCCTCTCTGCACGCCAGCCCGCCGCCACCCACCATGGCCACAGTTCA 62
Db 18  CGCCGACGAGACCCCTCTCTGCACGCCAGCCCGCCGCCACCCACCATGGCCACAGTTCA 77

QY 63  GCAGCTGGAGGAAGATGCGCGCTGGTGACAGCAAGAGCTTTGATGATACATGAAGGA 122
Db 78  GCAGCTGGAGGAAGATGCGCGCTGGTGACAGCAAGAGCTTTGATGATACATGAAGGA 137

QY 123 GCTAGAGTGGGAATAGCTTTTCGAAAATATGGGCGCAATGGCCAGCCAGATTGTATCAT 182
Db 138 GCTAGAGTGGGAATAGCTTTTCGAAAATATGGGCGCAATGGCCAGCCAGATTGTATCAT 197

QY 183 CACTTGTGATGTTAAAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGTT 242
Db 198 CACTTGTGATGTTAAAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGTT 257

QY 243 TTTCTGTACCTCGGAGAGAGTTTGAAGAACCAACAGCTGATGCGAAGAACTCAGAC 302
Db 258 TTTCTGTACCTCGGAGAGAGTTTGAAGAACCAACAGCTGATGCGAAGAACTCAGAC 317

QY 303 TGTCTGCAACTTTACAGATGGTGCAATGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 362
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Db      318  TGCTGCACTTTACAGATGTCATTTGTTTACGATCAGGATGGATGGAGGAAG 377
Qy      363  CACAATAACAAGAAAATTGAAGATGGAAAATTAGTGGTGGATGTGTATGAACAATGT 422
Db      378  CACAATAACAAGAAAATTGAAGATGGAAAATTAGTGGTGGATGTGTATGAACAATGT 437
Qy      423  CACCTGCTACTCGGATCTATGAAAAGTAGAATAAATAATTTCCATCATCATCTTTGGACAGGA 482
Db      438  CACCTGCTACTCGGATCTATGAAAAGTAGAATAAATAATTTCCATCATCATCTTTGGACAGGA 497
Qy      483  GTTAATTAAGAGAAATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCTCTTTCTTCT 542
Db      498  GTTAATTAAGAGAAATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCTCTTTCTTCT 557
Qy      543  TTTTCTTTTTCATCTACTGTTTCAATTTATCTTTATCATATAAACAATTTTACATGACGCTATTT 602
Db      558  TTTTCTTTTTCATCTACTGTTTCAATTTATCTTTATCATATAAACAATTTTACATGACGCTATTT 617
Qy      603  CAAAGTGTGTGGAATTAATGAGATCATCTCTTTGGTGTAAATAAATAATGTGTTGT 659
Db      618  CAAAGTGTGTGGAATTAATGAGATCATCTCTTTGGTGTAAATAAATAATGTGTTGT 674

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RESULT 3
BX385751
LOCUS
DEFINITION
BX385751 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DC028YA01 5-PRIME, mRNA sequence.
ACCESSION
BX385751
VERSION
BX385751.2 GI:46831903
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 662)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30457359.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .662
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC028YA01"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

```

FEATURES

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source
Query Match 99.0%; Score 655.4; DB 5; Length 662;
Best Local Similarity 99.4%; Pred. No. 1.8e-148;
Matches 656; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 3 CGCCGAGCGAGACCCCTCTCTGACGCCGCGCCGCCACCCACCATGCCACAGTTCA 62
Db 1 CGCGSAGGCGAGANCCCTCTCTGACGCCGCGCCGCCACCCACCATGCCACAGTTCA 60
Qy 63 GCAGCTGGAAGGAAGATGGCGCTGGTGGACAGCAAGAGCTTTGATGAATACATGAAGGA 122

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ORIGIN

```

Query Match 99.0%; Score 655.4; DB 5; Length 662;
Best Local Similarity 99.4%; Pred. No. 1.8e-148;
Matches 656; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 3 CGCCGAGCGAGACCCCTCTCTGACGCCGCGCCGCCACCCACCATGCCACAGTTCA 62
Db 1 CGCGSAGGCGAGANCCCTCTCTGACGCCGCGCCGCCACCCACCATGCCACAGTTCA 60
Qy 63 GCAGCTGGAAGGAAGATGGCGCTGGTGGACAGCAAGAGCTTTGATGAATACATGAAGGA 122

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Db      61  GCAGCTGGAAGGAAGATGGCGCTGGTGGACAGCAAGAGCTTTGATGAATACATGAAGGA 120
Qy      123  GCTAGGAGTGGGAATAGCTTTTGGAAAAATGGGCGCAATGGCCACGAGATTGTATCAT 182
Db      121  GCTAGGAGTGGGAATAGCTTTTGGAAAAATGGGCGCAATGGCCACGAGATTGTATCAT 180
Qy      183  CACTTGTGTATGTTAAAAAACCTCACCATATAAAAATGAGAGCACTTTGAAAAACAACAGTT 242
Db      181  CACTTGTGTATGTTAAAAAACCTCACCATATAAAAATGAGAGCACTTTGAAAAACAACAGTT 240
Qy      243  TTCTTTTACCCCTGGGAGAGAGTGTGAAGAAAACCAAGCTGATGGCAGAAAAAATCTCAGAC 302
Db      241  TTCTTTTACCCCTGGGAGAGAGTGTGAAGAAAACCAAGCTGATGGCAGAAAAAATCTCAGAC 300
Qy      303  TGTCTGCAACTTTTACAGATGTTGCTTTCAGCATCAGGAGTGGGATGGGAAGGAAAG 362
Db      301  TGTCTGCAACTTTTACAGATGTTGCTTTCAGCATCAGGAGTGGGATGGGAAGGAAAG 360
Qy      363  CACATTAACAAGAAAATTTGAAAGATGGGAAAATTTAGTGGTGGAGTGTGTATGAACAATGT 422
Db      361  CACAATAACAAGAAAATTTGAAAGATGGGAAAATTTAGTGGTGGAGTGTGTATGAACAATGT 420
Qy      423  CACCTGTACTCGGATCTATGAAAAGTAGAATAAATAATTTCCATCATCATCTTTGGACAGGA 482
Db      421  CACCTGTACTCGGATCTATGAAAAGTAGAATAAATAATTTCCATCATCATCTTTGGACAGGA 480
Qy      483  GTTAATTAAGAGAAATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCTCTTTCTTCT 542
Db      481  GTTAATTAAGAGAAATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCTCTTTCTTCT 540
Qy      543  TTTTCTTTTTCATCTACTGTTTCAATTTATCTTTATCATATAAACAATTTTACATGACGCTATTT 602
Db      541  TTTTCTTTTTCATCTACTGTTTCAATTTATCTTTATCATATAAACAATTTTACATGACGCTATTT 600
Qy      603  CAAAGTGTGTGGAATTAATGAGATCATCTCTTTGGTGTAAATAAATAATGTGTTGTGCT 662
Db      601  CAAAGTGTGTGGAATTAATGAGATCATCTCTTTGGTGTAAATAAATAATGTGTTGTGCT 660

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RESULT 4

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BX719235
LOCUS
DEFINITION
602690296F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822894 5',
mRNA sequence.
ACCESSION
BX719235
VERSION
BX719235.1 GI:13998422
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM10731 row: o column: 23
High quality sequence stop: 708.
Location/Qualifiers
1. .717
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

```

REFERENCE

```

AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES

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source

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/clone="IMAGE:4822894"
/lab_host="DH10B"
/note="NIH_MGC_97"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 99.0%; Score 655.2; DB 4; Length 717;
Best Local Similarity 99.5%; Pred. No. 2e-148;
Matches 657; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 CGCCGACGAGACCCCTCTCTGCAGCCAGCCCGCCGACCCACCATGGCCACAGTTCA 62
DB |||||
QY 38 CGCCGACGAGACCCCTCTCTGCAGCCAGCCCGCCGACCCACCATGGCCACAGTTCA 97
DB |||||
QY 63 CGAGCTGGAAGGAAGATGCGCTCTGTGACAGCAAGAGCTTTGATGAATACATCAAGGA 122
DB |||||
QY 98 CGAGCTGGAAGGAAGATGCGCTCTGTGACAGCAAGAGCTTTGATGAATACATCAAGGA 157
DB |||||
QY 123 GCTAGGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCCAAAGCAGATTTGATCAT 182
DB |||||
QY 158 GCTAGGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCCAAAGCAGATTTGATCAT 217
DB |||||
QY 183 CACTTGTGATGTAATAAACCCTCACATATAAATCTGAGAGCACTTTGAAAAACACAGTT 242
DB |||||
QY 218 CACTTGTGATGTAATAAACCCTCACATATAAATCTGAGAGCACTTTGAAAAACACAGTT 277
DB |||||
QY 243 TTCTGTACCTCGGAGAGAGCTTTGAGAAACACACAGCTGATGCAGAAAACTCAGAC 302
DB |||||
QY 278 TTCTGTACCTCGGAGAGAGCTTTGAGAAACACACAGCTGATGCAGAAAACTCAGAC 337
DB |||||
QY 303 TGCTGCAACTTTACAGATGGTGCAATGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 362
DB |||||
QY 338 TGCTGCAACTTTACAGATGGTGCAATGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 397
DB |||||
QY 363 CACATAACAGAAAAATTGAAGATGGGAAATTTAGTGTGGAGTGTGTATGAAACAATGT 422
DB |||||
QY 398 CACATAACAGAAAAATTGAAGATGGGAAATTTAGTGTGGAGTGTGTATGAAACAATGT 457
DB |||||
QY 423 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTTCCATCATCTTTGGACAGA 482
DB |||||
QY 458 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTTCCATCATCTTTGGACAGA 517
DB |||||
QY 483 GTTAATTAAAGAGATGACCAAGCTCAGTTTCAATGAGCAAAATCTCCATCTGTTCTTCT 542
DB |||||
QY 518 GTTAATTAAAGAGATGACCAAGCTCAGTTTCAATGAGCAAAATCTCCATCTGTTCTTCT 577
DB |||||
QY 543 TTTTCTTTTTCATATCTGTGTTCAATTTTATCATATAAACAATTTTACATGACGATTTT 602
DB |||||
QY 578 TTTTCTTTTTCATATCTGTGTTCAATTTTATCATATAAACAATTTTACATGACGATTTT 637
DB |||||
QY 603 CAAAGTGTCTGGATTAATTAGGATCATCCCTTTGTTTAAATAAATAAATGTTTGTGCT 662
DB |||||
QY 638 CAAAGTGTCTGGATTAATTAGGATCATCCCTTTGTTTAAATAAATAAATGTTTGTGCT 697
DB |||||

RESULT 5

LOCUS BG678687 820 bp mRNA linear EST 01-May-2001
DEFINITION 602624485F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4749429 5',
mRNA sequence.
ACCESSION BG678687
VERSION BG678687.1 GI:13910084
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 820)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1AM10602 row: j column: 22
High quality sequence stop: 682.

FEATURES

source

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/clones="IMAGE:4749429"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn4"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN

Query Match 98.3%; Score 650.8; DB 4; Length 820;
Best Local Similarity 99.7%; Pred. No. 2.4e-147;
Matches 652; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 CGCAGACCCCTCTGCGACGCGCCGCGCCGCCACCATGGCCACAGTTTCAGCAGCT 68
DB 1 CGCAGACCCCTCTGCGACGCGCGCCGCGCCGCCACCATGGCCACAGTTTCAGCAGCT 60
QY 69 GGAAGAGATGGCGCCCTGCTGGACAGCAAAAGGCTTTGATGAATACATCAAGAGCTAGG 128
DB 61 GGAAGAGATGGCGCCCTGCTGGACAGCAAAAGGCTTTGATGAATACATCAAGAGCTAGG 120
QY 129 AGTGGAAATAGCTTTGCCAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCCTTG 188
DB 121 AGTGGAAATAGCTTTGCCAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCCTTG 180
QY 189 TGATGGTAAACCTCCACCATATAAATCTGAGAGCACTTTGAAAAACAACACAGTTTCTTG 248
DB 181 TGATGGTAAACCTCCACCATATAAATCTGAGAGCACTTTGAAAAACAACACAGTTTCTTG 240
QY 249 TACCCTGGGAGAGATTTGAAGAAACCAACAGCTGATGGCGAAAAAATCTCAGACTGTCTG 308
DB 241 TACCCTGGGAGAGATTTGAAGAAACCAACAGCTGATGGCGAAAAAATCTCAGACTGTCTG 300
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DB 301 CAACCTTTACAGATGGTGCAATTTGTTTCAGATCAGAGTGGGATGGGAAGGAAGCAAT 360
QY 369 AACAGAAAAATTTGAAGATGGGAATTTAGTGTGGAGTGTGTCATGAACAATGTCCCTTG 428
DB 361 AACAGAAAAATTTGAAGATGGGAATTTAGTGTGGAGTGTGTCATGAACAATGTCCCTTG 420
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DB 421 TACTCGGATCTATGAAAAAGTAGAATAAAAAATTTCCATCATCTTTGGACAGGAGTTAAT 480
QY 489 TAAGAGAAATGACCAAGCTCAGTTTCAATGAGCAAAATCTCCATCTGTTCTTTCTTTT 548
DB 481 TAAGAGAAATGACCAAGCTCAGTTTCAATGAGCAAAATCTCCATCTGTTCTTTCTTTT 540


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QY 549 TTTCATTACTGTGTTCAATATCTTTATCATTAACATTTTACATGCGAGCTATTTCAAAGT 608
DB 541 TTTCATTACTGTGTTCAATATCTTTATCATTAACATTTTACATGCGAGCTATTTCAAAGT 600
QY 609 GTGTGCGATTAATAGGATCATCCCTTGTGTTAAATAAATAAATGTTGTGCT 662
DB 601 GTGTGCGATTAATAGGATCATCCCTTGTGTTAAATAAATAAATGTTGTGCT 654

RESULT 6
AV727829 786 bp mRNA linear EST 17-OCT-2000
AV727829 HTC Homo sapiens cDNA clone HTCWG07 5', mRNA sequence.
AV727829
AV727829.1 GI:10837250
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA HTC clones
Unpublished (2000)
CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
LOCATION/Qualifiers
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XhoI"

ORIGIN
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Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 8 AGCGAGACCCCTCTCTGCGAGCGCCGCGCCGACCCACCAATGCGCAGTTTCAGCAGC 67
DB 1 AGCGAGACCCCTCTCTGCGAGCGCCGCGCCGACCCACCAATGCGCAGTTTCAGCAGC 60
QY 68 TCGAAGGAGAGTGGCCCTGTTGGACAGCAAGGCTTTTCATGATATACATGAAGGAGCTAG 127
DB 61 TCGAAGGAGAGTGGCCCTGTTGGACAGCAAGGCTTTTCATGATATACATGAAGGAGCTAG 120
QY 128 GAGTGGGAATAGCTTTGCGAAATAATGGCGCAATGGCCAGGAGGAGGAGGAGCTAT 187
DB 121 GAGTGGGAATAGCTTTGCGAAATAATGGCGCAATGGCCAGGAGGAGGAGGAGCTAT 180
QY 188 GTGATGGTAAAAACCTCAGCATAAACTGAGAGCACTTTGAAACCAACACAGTTTCTT 247
DB 181 GTGATGGTAAAAACCTCAGCATAAACTGAGAGCACTTTGAAACCAACACAGTTTCTT 240
QY 248 GTACCTGGGAGAGTTTGAAGAAACACAGCTGATGCGAGAAACCTCAGAGCTGCT 307
DB 241 GTACCTGGGAGAGTTTGAAGAAACACAGCTGATGCGAGAAACCTCAGAGCTGCT 300

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QY 308 GCAACTTTACAGATGGTGCATTTGGTTTACAGATCAGAGTGGATGGGAAGGAAGCACAA 367
DB 301 GCAACTTTTACAGATGGTGCATTTGGTTTACAGATCAGAGTGGATGGGAAGGAAGCACAA 360
QY 368 TAAACAAGAAAATTTGAAAGATGGAAATTTAGTGGTGGAGTGTGTATGAACAATGTCACT 427
DB 361 TAAACAAGAAAATTTGAAAGATGGAAATTTAGTGGTGGAGTGTGTATGAACAATGTCACT 420
QY 428 GTACTCGGATCTATGAAAAGTAGAATAAAAAATTCATCATCATCTTTTGGACAGGAGTTAA 487
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QY 488 TTAAGAAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCATCTTTCTTTT 547
DB 481 TTAAGAAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCATCTTTCTTTT 540
QY 548 TTTTCAATTACTGTGTTCAATTATCTTTATCATTAACATTTTACATGCGAGCTATTTCAAAG 607
DB 541 CTTTCAATTACTGTGTTCAATTATCTTTATCATTAACATTTTACATGCGAGCTATTTCAAAG 600
QY 608 TGTGTTGGATTAATTAGGATCATCCCTTGTGTTAAATAAATAAATGTTGTGCT 662
DB 601 TGTGTTGGATTAATTAGGATCATCCCTTGTGTTAAATAAATAAATGTTGTGCT 655

RESULT 7
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mRNA sequence.
BG715536
BG715536.1 GI:13994723
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.mci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10686 row: c column: 11
High quality sequence stop: 687.
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(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

FEATURES
source
location/Qualifiers
1..708
/organism="Homo sapiens"
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/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

```

Query Match 97.3%; Score 644.2; DB 4; Length 708;
Best Local Similarity 99.4%; Pred. No. 9.5e-146;
Matches 657; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 CGCCGACGACGACCCCTCTCTGCGCCGACGCGCCGCGCCGACCCACCATGCGCCACAGTTCA 62
DB 20 CGCCGACGACGACCCCTCTCTGCGCCGACGCGCCGCGCCGACCCACCATGCGCCACAGTTCA 79

QY 63 GCAGCTGGAAGGAGATGCGCGCTGCTGGACAGCAAGAGCTTTGATGAATACATGAAGA 122
DB 80 GCAGCTGGAAGGAGATGCGCGCTGCTGGACAGCAAGAGCTTTGATGAATACATGAAGA 139

QY 123 GCTAGGAGTGGGATAGCTTTGCGAAGAAATGGCGCAATGGCCAGCCAGATTTGTATCAT 182
DB 140 GCTAGGAGTGGGATAGCTTTGCGAAGAAATGGCGCAATGGCCAGCCAGATTTGTATCAT 199

QY 183 CACTTGTGATGTTAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACACAGTT 242
DB 200 CACTTGTGATGTTAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACACAGTT 259

QY 243 TTTCTGTACCTCGGAGAGAGTTTGAAGAAACCAACAGCTGATGCGAGAAACCTCAGAC 302
DB 260 TTTCTGTACCTCGGAGAGAGTTTGAAGAAACCAACAGCTGATGCGAGAAACCTCAGAC 319

QY 303 TGTCTGCACTTTACAGATGCTGCAATGGTTTCAGCATCAGGAGTGGGATGGGAGGAAG 362
DB 320 TGTCTGCACTTTACAGATGCTGCAATGGTTTCAGCATCAGGAGTGGGATGGGAGGAAG 379

QY 363 CACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGTGGAGTGTGTCATGAACAATGT 422
DB 380 CACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGTGGAGTGTGTCATGAACAATGT 439

QY 423 CACTGTACTCGGATTTAATGAGATCATCCCTTTGGTTAATAAATAATGTTTGTGC 661
DB 620 TCAAAAGTGTGGGATTAATAGGATCATCCCTTGGTTAATAAATAATGTTTGTGC 679

QY 662 T 662
DB 680 T 680

RESULT 8
BU943612
LOCUS
DEFINITION
AGENCY 10545886 NIH_MGC_126 Homo sapiens cdna clone
IMAGE: 6723797 5', mRNA sequence.

ACCESSION
BU943612
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 748)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI

cdna Library Preparation: Michael Brownstein Laboratory
cdna Library Arrayed by: The I.M.A.G.E. Consortium (ILLN).
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLN at:
<http://image.llnl.gov>
Plate: LLCM3037 row: p column: 04
High quality sequence stop: 582.
Location/Qualifiers
1. 748
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/note="Vector: pNMR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3',
adaptors were used in cloning as follows:
5'-AAGCAGGTGATCAACGAGAGTGGCCATTAGCGCGG-3' and
5'-ATTCTAGAGCGGAGCGCGGCACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5-1
kb size fraction (other fractions present in NIH_MGC_127
and NIH_MGC_128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
Library."

FEATURES
source

ORIGIN

Query Match 97.3%; Score 643.8; DB 5; Length 748;
Best Local Similarity 99.5%; Pred. No. 1.2e-145;
Matches 656; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3 CGCCGACGACGACCCCTCTCTGCGCGCGCGCGCGCGCCACCATGCGCCACAGTTCA 62
DB 20 CGCCGACGACGACCCCTCTCTGCGCGCGCGCGCGCGCCACCATGCGCCACAGTTCA 79

QY 63 GCAGCTGGAAGGAGATGCGCGCTGCTGGACAGCAAGAGCTTTGATGAATACATGAAGA 122
DB 80 GCAGCTGGAAGGAGATGCGCGCTGCTGGACAGCAAGAGCTTTGATGAATACATGAAGA 139

QY 123 GCTAGGAGTGGGATAGCTTTGCGAAGAAATGGCGCAATGGCCAGCCAGATTTGTATCAT 182
DB 140 GCTAGGAGTGGGATAGCTTTGCGAAGAAATGGCGCAATGGCCAGCCAGATTTGTATCAT 199

QY 183 CACTTGTGATGTTAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACACAGTT 242
DB 200 CACTTGTGATGTTAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACACAGTT 259

QY 243 TTTCTGTACCTCGGAGAGAGTTTGAAGAAACCAACAGCTGATGCGAGAAACCTCAGAC 302
DB 260 TTTCTGTACCTCGGAGAGAGTTTGAAGAAACCAACAGCTGATGCGAGAAACCTCAGAC 319

QY 303 TGTCTGCACTTTACAGATGCTGCAATGGTTTCAGCATCAGGAGTGGGATGGGAGGAAG 362
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QY 363 CACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGTGGAGTGTGTCATGAACAATGT 422
DB 380 CACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGTGGAGTGTGTCATGAACAATGT 439

QY 423 CACTGTACTCGGATTTAATGAGATCATCCCTTTGGTTAATAAATAATGTTTGTGC 482
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 Qy 543 TTTTCTTTTCACTACTGCTGCTCAATATCTTTATCATAAACATTTTACATGCGAGCTATTT 602
 Db 560 TTTTCTTTTCACTACTGCTGCTCAATATCTTTATCATAAACATTTTACATGCGAGCTATTT 619
 Qy 603 CAAAGTGTGTTGGATTAATAGATCATCCCTTTGGTTTAAATAAATGCTGTTGTGC 661
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RESULT 9
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 ACCESSION BM789868
 VERSION 1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 666)
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 8 row: D column: 02
 High quality sequence stop: 666.
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 /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli top10F' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

FEATURES

source
 1..666
 /organism="Homo sapiens"
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 Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli top10F' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 97.1%; Score 643; DB 4; Length 666;
 Best Local Similarity 99.8%; Pred. No. 1.8e-145;
 Matches 654; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

FEATURES

Location/Qualifiers

Qy 3 CGCCGACGACAGCCCTCTCTGCAGCCGACCCCGCCGACCCACCATGGCCACAGTTCA 62
 Db 13 CGCCGACGACAGCCCTCTCTGCAGCCGACCCCGCCGACCCACCATGGCCACAGTTCA 72
 Qy 63 CGAGCTGGAAGGAGATGGCGCTGCTGGACAGCAAGGCTTGTGATACATGAAGA 122
 Db 73 GCAGCTGGAAGGAGATGGCGCTGCTGGACAGCAAGGCTTGTGATACATGAAGA 132
 Qy 123 GCTAGAGTGGGAATAGCTTTTCGGAATAATGGCGCAATGGCCAAAGCCAGATTGTATCAT 182
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 Qy 183 CACTTTGTATGCTTAAACCTCACCATAAATCTGAGAGCACTTTGAAAACACACAGTT 242
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 Db 253 TTCTTTGATACCTCCCTGGGAGAGAGTGTGAAGAAACACAGCTGATGGCAGAAAACTCAGAC 312
 Qy 303 TGTCTGCAACTTTTACAGATGGTGCAATGGTTCAGATCAGGAGTGGGATGGGAAGAAAG 362
 Db 313 TGTCTGCAACTTTTACAGATGGTGCAATGGTTCAGATCAGGAGTGGGATGGGAAGAAAG 372
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ACCESSION BU601920
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 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 843)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 Location/Qualifiers

source

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/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCAGTGGTATCAACGACGAGTGGCCATTACGGCGGG-3' and
5'-ATTAGAGCGCGGCGGCCGACATG-DT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH_MGC_141).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."
ORIGIN
Query Match          96.8%; Score 640.8; DB 5; Length 843;
Best Local Similarity 98.2%; Pred. No. 6.5e-145;
Matches 648; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 3 CGCCGACGAGACCCCTCTCTGACGCGACGCCGCCGCCGCCACCCACCATGGCCACAGTTCA 62
DB 18 CGCCGACGAGACCCCTCTCTGACGCGCAGCCGCCGCCGCCACCCACCATGGCCACAGTTCA 77
QY 63 GCAGCTGGAAGGAAGATGCGCTCTGTCAGACAGAAAGCTTTGTATGAATACATGAAGA 122
DB 78 GCAGCTGGAAGGAAGATGCGCTCTGTCAGACAGAAAGCTTTGTATGAATACATGAAGA 137
QY 123 GCTAGAGTGGGAATAGCTTTTCGGAATATGGCCCAATGGCCCAATGGCCCAATGGTATCAT 182
DB 138 GCTAGAGTGGGAATAGCTTTTCGGAATATGGCCCAATGGCCCAATGGCCCAATGGTATCAT 197
QY 183 CACTTGTGATGTAAACCACTCACCATAAACTGAGACGACTTTGAAACCAACACAGTT 242
DB 198 CACTTGTGATGTAAACCACTCACCATAAACTGAGACGACTTTGAAACCAACACAGTT 257
QY 243 TTCTTGTACCTTGGAGAGAACTTTGAAGAAACCAACAGCTGATGCGAGAAACCTCAGAC 302
DB 258 TTCTTGTACCTTGGAGAGAACTTTGAAGAAACCAACAGCTGATGCGAGAAACCTCAGAC 317
QY 303 TGCTTGCACCTTTACAGATGGTGCATTTGGTTTCCAGCATCAGGATGGGATGGGAAGAAAG 362
DB 318 TGCTTGCACCTTTACAGATGGTGCATTTGGTTTCCAGCATCAGGATGGGATGGGAAGAAAG 377
QY 363 CACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTATCAACAAATGT 422
DB 378 CACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTATCAACAAATGT 437
QY 423 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTTCCATCATCATCTTTGGACAGA 482
DB 438 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTTCCATCATCATCTTTGGACAGA 497
QY 483 GTTAATTAGAGAAATGACCAAGCTCAGTTCAATGAGCAATCTCCATCTGTTCTTTCT 542
DB 498 GTTAATTAGAGAAATGACCAAGCTCAGTTCAATGAGCAATCTCCATCTGTTCTTTCT 557
QY 543 TTTTCTTTTTCATTAATGTTTCAATTAATCTTTTATCAATAAATTTTATCATGCAAGTATTT 602
DB 558 TTTTCTTTTTCATTAATGTTTCAATTAATCTTTTATCAATAAATTTTATCATGCAAGTATTT 617
QY 603 CAAAGTGTGTTGGAATTAATGAGATCATCCCTTTGGTGTAAATAAATGTTGTTGTGCT 662
DB 618 CAAAGTGTGTTGGAATTAATGAGATCATCCCTTTGGTGTAAATAAATGTTGTTGTGCT 677
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RESULT 11

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AV724494
LOCUS          AV724494
DEFINITION    HTB Homo sapiens CDNA clone HTBAYF07 5', mRNA sequence.
ACCESSION     AV724494
VERSION       AV724494.1 GI:10828936
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 656)
AUTHORS       Gu, Y., Peng, Y., Song, H., Huang, Q., Yang, Y., Gao, G., Xiao, H., Xu, X.,
              Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z., Zeng, L.,
              Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R.,
              Chen, J., Chen, Z. and Han, Z.
              Homo sapiens CDNA HTB clones
              Unpublished (2000)
              Contact: Zeguang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919 (ex. 45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.
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                     /tissue_type="Hypothalamus"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="HTB"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
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Query Match          96.7%; Score 640.4; DB 1; Length 656;
Best Local Similarity 99.8%; Pred. No. 7.8e-145;
Matches 641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 GCCGACGAGACCCCTCTCTGACGCGCAGCCGCCGCCGCCACCCACCATGGCCACAGTTCA 63
DB 1 GCCGACGAGACCCCTCTCTGACGCGCAGCCGCCGCCGCCACCCACCATGGCCACAGTTCA 60
QY 64 CAGCTGGGAAGGAAGATGGCGCTGTGGACAGCAAGGCTTTGTATGAATACATGAAGGAG 123
DB 61 CAGCTGGGAAGGAAGATGGCGCTGTGGACAGCAAGGCTTTGTATGAATACATGAAGGAG 120
QY 124 CTAGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCCCAAGCCAGATTGTATCATC 183
DB 121 CTAGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCCCAAGCCAGATTGTATCATC 180
QY 184 ACTTGTGATGTAAACCACTCACCATAAACTGTAGAGCACTTTGAAACCAACACAGTTT 243
DB 181 ACTTGTGATGTAAACCACTCACCATAAACTGTAGAGCACTTTGAAACCAACACAGTTT 240
QY 244 TCTTGTACCTTGGGAGAGAGCTTTTGAAGAAACCAACAGCTGTGGCAGAAAACTCAGACT 303
DB 241 TCTTGTACCTTGGGAGAGAGCTTTTGAAGAAACCAACAGCTGTGGCAGAAAACTCAGACT 300
QY 304 GTCTGCAACTTTTACAGATGGTGCATTTGTTTCCAGCATCAGGATGGGATGGGAAGGAAAGC 363
DB 301 GTCTGCAACTTTTACAGATGGTGCATTTGTTTCCAGCATCAGGATGGGATGGGAAGGAAAGC 360
QY 364 ACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTATGAACATGTC 423
DB 361 ACAATAACAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTATGAACATGTC 420
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3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Seares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pMT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGGCATGGCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FTI
TAG_SEQ=GGCCATGGCG"

ORIGIN

Query Match 95.6%; Score 632.8; DB 6; Length 654;
Best Local Similarity 99.7%; Pred. No. 5.5e-143;
Matches 634; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 27 CGCCAGCCCGCCGACCCACCATGCGCCAGTTCAGCAGCTGGAAGGAGATGGCGCT 86
DB 654 CGCCAGCCCGCCGACCCACCATGCGCCAGTTCAGCAGCTGGAAGGAGATGGCGCT 595

QY 87 GGTGGACAGCAAGGCTTTGATGATACATGAGGAGCTAGGAGTGGGATAGCTTTGGC 146
DB 594 GGTGGACAGCAAGGCTTTGATGATACATGAGGAGCTAGGAGTGGGATAGCTTTGGC 535

QY 147 AAAATGGGCGCAATGGCAAGCAGATTGTATCATCTGTGTATGATGTTAAACCTCAC 206
DB 534 AAAATGGGCGCAATGGCAAGCAGATTGTATCATCTGTGTATGATGTTAAACCTCAC 475

QY 207 CATAAAACGTGAGACACTTTGAAAACACACAGTTTCTGTACCTGGGAGAGATT 266
DB 474 CATAAAACGTGAGACACTTTGAAAACACACAGTTTCTGTACCTGGGAGAGATT 415

QY 267 TGAAGAAACACAGCTGTATGGAGAAACACTCAGACTGTCTGCAACTTTACAGATGGTGC 326
DB 414 TGAAGAAACACAGCTGTATGGAGAAACACTCAGACTGTCTGCAACTTTACAGATGGTGC 355

QY 327 ATTGGTTACGATCAGGAGTGGGATGGGAGGAAAGCAAAATAACAAGAAATTTGAAGA 386
DB 354 ATTGGTTACGATCAGGAGTGGGATGGGAGGAAAGCAAAATAACAAGAAATTTGAAGA 295

QY 387 TGGGAATTTAGTGGTGGATGTCTATGACATGTCACTGTCTACTCGATCTATGAAA 446
DB 294 TGGGAATTTAGTGGTGGATGTCTATGACATGTCACTGTCTACTCGATCTATGAAA 235

QY 447 AGTAGAATAAAATTCATCATCTTTCAGCAGGAGTTAAATTAAGAGATGACCAAGCT 506
DB 234 AGTAGAATAAAATTCATCATCTTTCAGCAGGAGTTAAATTAAGAGATGACCAAGCT 175

QY 507 CAGTTCAATGAGCAAAATCCATCTGTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCAA 566
DB 174 CAGTTCAATGAGCAAAATCCATCTGTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCAA 115

QY 567 TTATCTTTTATCAATAACATTTTACATGACCTATTTCAAAGTGTGTGGAATTAATAGGA 626
DB 114 TTATCTTTTATCAATAACATTTTACATGACCTATTTCAAAGTGTGTGGAATTAATAGGA 55

QY 627 TCATCCCTTTGGTTAATAATAAATGTTTGTGCT 662
DB 54 TCATCCCTTTGGTTAATAATAAATGTTTGTGCT 19

RESULT 15

BU532649

LOCUS

DEFINITION

BU532649 799 bp mRNA linear EST 13-SEP-2002
AGENCOURT_10204551 NIH_MGC_126 Homo sapiens cDNA clone
IMAGE:6558459 5', mRNA sequence.

ACCESSION

BU532649

VERSION

BU532649.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: NCI

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2728 row: c column: 03

High quality sequence stop: 541.

FEATURES

Location/Qualifiers

1..799

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6558459"

/tissue_type="mixed (pool of 40 RNAs)"

/lab_host="DH10B (T1-phage-resistant)"

/clone_lib="NIH_MGC_126"

/note="Vector: pDNR-LIB; Site 1: Sfil (ggccatattggcc);

Site 2: Sfil (ggccgctcgcc); Double-stranded cDNA was

prepared from a pool of 40 cell line polyA+ RNAs (bladder

- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,

kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -

5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,

salivary gland - 1.3%, and skin - 2.3%). 5' and 3'

adaptors were used in cloning as follows:

5'-AAGCAGTGTGATCAAGCAGATGGCCATTCGCGCGG-3' and

5'-ATTCTAGAGCGCGGCGCGCCAGATG-DT(30)NN-3'. Full-length

enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.5-1

kb size fraction (other fractions present in NIH MGC 127

and NIH MGC 128). Library created in the laboratory of T.

Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 95.5%; Score 632.4; DB 5; Length 799;
Best Local Similarity 99.5%; Pred. No. 7.1e-143;
Matches 655; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 3 CGCCAGCGAGACCCCTCTCTGACGCGCAGCCCGCGCCGCCACCCACCATGGCCACAGTTCA 62
DB 17 CGCCAGCGAGACCCCTCTCTGACGCGCAGCCCGCGCCGCCACCCACCATGGCCACAGTTCA 76

QY 63 CGAGCTGGAAGGAAGATGCGCTGTGGACAGCAAGGCTTTGATGATACATGAAGA 122
DB 77 CGAGCTGGAAGGAAGATGCGCTGTGGACAGCAAGGCTTTGATGATACATGAAGA 136

QY 123 GCTAGGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCCAGCCAGCAGATTGTATCAT 182
DB 137 GCTAGGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCCAGCAGATTGTATCAT 196

QY 183 CACTTGTGATGTGTAATAAACCTTCCATATAAACTGAGAGCACTTTGAAAAAACACAGATT 242
DB 197 CACTTGTGATGTGTAATAAACCTTCCATATAAACTGAGAGCACTTTGAAAAAACACAGATT 256

QY 243 TTTCTTGTACCTTGGGAGAGAGTTTGAAGAAACACACAGCTGATGCAGAAAACTCAGAC 302
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QY 303 TGTCTGCAACTTTACAGATGGTGCATTGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 362
Db |||||
QY 317 TGTCTGCAACTTTACAGATGGTGCATTGGTTCCAGCATCAGGAGTGGGATGGGAAGAAAG 376
Db |||||
QY 363 CACAATAACAAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCTCATCAACAATGT 422
Db |||||
QY 377 CACATTAACAAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCTCATGAACAATGT 436
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QY 423 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCACTTTTGGACAGGA 482
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QY 437 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCACTTTTGGACAGGA 496
Db |||||
QY 483 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCCCATACTGTTCTTCT 542
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QY 497 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCCCATACTGTTCTTCT 556
Db |||||
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Db |||||
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Db |||||
QY 603 CAAAGTGT-GTTGGATTAATTAGGATCAT-CCCTTTGGTTAATAAATAAATGTGTTTG 658
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Search completed: July 12, 2005, 21:11:53
Job time : 2590.24 secs

Result No.	Query			DB	ID	Description
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2	662	100.0	662	6	CQ861699	Sequence
3	662	100.0	662	6	AX224147	Sequence
4	662	100.0	662	9	HUMFABPHA	
5	660	99.7	661	6	CQ719340	Sequence
6	660	99.7	680	9	BC019385	Human sapi
7	660	99.7	720	6	BD203735	Human nuc
8	660	99.7	720	6	AX014890	Sequence
9	658	99.4	706	9	BC070303	Homo sapi
10	649	98.0	1072	6	AX281734	Sequence
11	645	97.4	645	6	CQ729706	Sequence
12	645	97.4	156734	9	AP000640	Homo sapi
13	645	97.4	180726	2	AC090343	Homo sapi
14	645	97.4	195396	2	AC021809	Homo sapi
15	642.4	97.0	661	6	CQ725017	Sequence
16	625.6	94.5	199882	9	AL354720	Human DNA
17	623.2	94.1	194150	2	AC148825	Pan trogl
18	618.6	93.4	651	6	CQ724062	Sequence
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LOCUS      CQ861699                662 bp      DNA      linear      PAT 10-SEP-2004
DEFINITION Sequence 332 from Patent WO2004072265.
ACCESSION  CQ861699
VERSION     CQ861699.1  GI:51982688
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Burczynski, M., Twine, N., Dornier, A. J. and Trepicchio, W. L.
TITLE     METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i
JOURNAL   Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dornier, Andrew J. (US); Trepicchio, William L. (US)
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.7e-146;
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Qy      481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
Db      481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
Qy      541 CTTTTTTTTTCACTACTGTGTTCAATTTATCTTTATCAATAAATTTTACATGCAGCTAT 600
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Qy      601 TTCAAAGTGTGGTAAATTTAGGATCATCCCTTTGGTAAATAAATGTTTGTG 660
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Qy      661 CT 662
Db      661 CT 662

RESULT 3
LOCUS      AX224147                662 bp      DNA      linear      PAT 10-SEP-2001
DEFINITION Sequence 4 from Patent WO0160384.
ACCESSION  AX224147
VERSION     AX224147.1  GI:15554410
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS   Hotamisligil, G. S.
TITLE     Inhibition of mal-1, the keratinocyte lipid binding protein
JOURNAL   Patent: WO 0160384-A 4 23-AUG-2001;
PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
FEATURES   Location/Qualifiers
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            1..662
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ORIGIN
Query Match      100.0%; Score 662; DB 6; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.7e-146;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ACCGGCGACGACAGCCCTCTCTGACGCCAGCCGCCGCCGCCGCCGCCAGGTT 60
Db      1 ACCGGCGACGACAGCCCTCTCTGACGCCAGCCGCCGCCGCCGCCGCCAGGTT 60
Qy      61 CAGCAGCTCGAAGGAAGATGGCGCTCTGTCAGCGCAGCAAGAGGCTTTGATGAATACATGAAG 120
Db      61 CAGCAGCTCGAAGGAAGATGGCGCTCTGTCAGCGCAGCAAGAGGCTTTGATGAATACATGAAG 120
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Db 121 GAGCTAGGAGTGGGAATAGCTTTTCGAAAAATGGGGCGCAATGGCCAGCCAGCATTTGTATC 180
QY 181 ATCACTTGTGATGGTAAACCTTCCACATATAAAGTGGAGGACCTTTGAAAAACACACACAG 240
Db 181 ATCACTTGTGATGGTAAACCTTCCACATATAAAGTGGAGGACCTTTGAAAAACACACACAG 240
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Db 241 TTTTCTTGTAACCTGGGAGAGAGTTTGAAGAAACACACAGCTGATGCGAGAAAACTCAG 300
QY 301 ACTGTCGCAACTTACAGATGGTGCATTTGGTTACGATCAGGAGTGGAGTGGGAAGGAA 360
Db 301 ACTGTCGCAACTTACAGATGGTGCATTTGGTTACGATCAGGAGTGGAGTGGGAAGGAA 360
QY 361 AGCACAATACAGAAAAATTTGAAGAGTGGAAAAATTTAGTGGTGGAGTGTGCATGAACAAT 420
Db 361 AGCACAATACAGAAAAATTTGAAGAGTGGAAAAATTTAGTGGTGGAGTGTGCATGAACAAT 420
QY 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAG 480
Db 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAG 480
QY 481 GAGTTAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTTTGCTTT 540
Db 481 GAGTTAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTTTGCTTT 540
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Db 541 CTTTCTTTTTCATTAAGTGTGTTCAATTAATCTTTTATCAATAAATTTTACATGCGCTAT 600
QY 601 TTTCAAGTGTGTTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTGTG 660
Db 601 TTTCAAGTGTGTTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTGTG 660
QY 661 CT 662
Db 661 CT 662
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RESULT 4
HUMFABPHA 662 bp mRNA linear PRI 31-DEC-1994
LOCUS Human fatty acid binding protein homologue (PA-FABP) mRNA, complete cds.
ACCESSION M94856
VERSION M94856.1 GI:182353
KEYWORDS fatty acid binding protein homologue.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 662)
Madsen, P., Rasmussen, H.H., Leffers, H., Honore, B. and Celis, J.E.
Molecular cloning and expression of a novel keratinocyte protein (psoriasis-associated fatty acid-binding protein [PA-FABP]) that is highly up-regulated in psoriatic skin and that shares similarity to fatty acid-binding proteins
J. Invest. Dermatol. 99 (3), 299-305 (1992)
92381332
MEDLINE 1512466
COMMENT Original source text: Homo sapiens (tissue library: lambda gt11) adult epidermis cDNA to mRNA.
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/cell_line="unfractionated non-cultured keratinocyte"

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ORIGIN chromosome 17.
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Query Match 100.0%; Score 662; DB 9; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.7e-146;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGCGCAGCAGACCCCTCTCTGCACGCGCAGCCCGCCGCCACCCACCATGGCCACAGTT 60
Db 1 ACCGCGCAGCAGACCCCTCTCTGCACGCGCAGCCCGCCGCCACCCACCATGGCCACAGTT 60
QY 61 CAGCAGCTGGAAGGAAGATGGCGCTTGGTGGACAGCAAAAGGCTTTGATGAATACATGAAG 120
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QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGGGCGCAATGGCCAGCCAGATTTGTATC 180
Db 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGGGCGCAATGGCCAGCCAGATTTGTATC 180
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QY 481 GAGTTAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTTTGCTTT 540
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Db 601 TTTCAAGTGTGTTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTGTG 660
QY 661 CT 662
Db 661 CT 662
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RESULT 5
CQ719340

LOCUS CQ719340 661 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence S274 from Patent WO02068579.
ACCESSION CQ719340
VERSION CQ719340.1 GI:42280197
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
REFERENCE Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Kits, such as nucleic acid arrays, comprising a majority of
TITLE humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 5274 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 99.7%; Score 660; DB 6; Length 661;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCGACGAGACCCCTCTCTGACGCCACGCCGCCGCCGCCACCCACCATGCGCCACAGTTCA 62
Db 2 CGCCGAGCGAGACCCCTCTCTGACGCCACGCCGCCGCCGCCACCCACCATGCGCCACAGTTCA 61
QY 63 GCAGCTGGAAGGAAGATGCGCGCTGCTGACGACGAAAGCCTTTGATGATATCATGAGGA 122
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Db 122 GCTAGAGTGGGAATAGCTTTTCGAAAAATGGCGCAATGGCGCAAGCCAGATTTGTATCAT 181
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QY 543 TTTTCTTTTTCATTACTGTGTCAATTTATCTTTATCATAAACATTTTACATGACGCTATTT 602
Db 542 TTTTCTTTTTCATTACTGTGTCAATTTATCTTTATCATAAACATTTTACATGACGCTATTT 601
QY 603 CAAAGTGTGTGGAATTAATAGGATCATCCCTTGTGTTAAATAAATGTTTGTGCT 662
Db 602 CAAAGTGTGTGGAATTAATAGGATCATCCCTTGTGTTAAATAAATGTTTGTGCT 661

RESULT 6

BC019385 680 bp mRNA linear PRI 29-JUN-2004
LOCUS Homo sapiens fatty acid binding protein 5 (psoriasis-associated),
DEFINITION mRNA (cDNA clone MGC:9003 IMAGE:3862100), complete cds.
ACCESSION BC019385
VERSION BC019385.2 GI:34783324
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 680)
REFERENCE Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
AUTHORS Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shvachenko, Y.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shvachenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnurich, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE Strausberg, R.
AUTHORS Direct Submission
TITLE Submitted (19-DEC-2001) National Institutes of Health, Mammalian
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT On Sep 16, 2003 this sequence version replaced gi:18043065.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleeged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 21 Row: 9 Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4557580.
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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ORIGIN

Query Match 99.7%; Score 660; DB 9; Length 680;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCGACGAGACCCCTCTCTGACCGCAGCCGCGCCGACCCACCATGGCCACAGTTCA 62
DB 1 CGCCGACGAGACCCCTCTCTGACCGCAGCCGCGCCGACCCACCATGGCCACAGTTCA 60
QY 63 GCAGCTGGAAGGAGATGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAGGA 122
DB 61 GCAGCTGGAAGGAGATGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAGGA 120
QY 123 GCTAGAGTGGGAATAGCTTTTGGAAAAATGGCGCAATGGCCAGCCAGATTGTATCAT 182
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QY 183 CACTTGTGATGTTAAACCTCACCATAAACTGAGAGCATTTCAGAACACACAGTT 242
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QY 243 TTCTGTACCTGGGAGAGAGTTTGAAGAAACACAGCTGTAGTGGCAGAAAACTCAGAC 302
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QY 303 TGTCTGCAACTTTACAGATGGTGCTATGTTTACGATACAGGAGTGGGAGGAGAAAG 362
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DB 361 CACATAACAGAAATTTGAAGATGGGAAATTTAGTGGTGGAGTGTCATGACAACTGT 420
QY 423 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTTGGACAGGA 482
DB 421 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTTGGACAGGA 480
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DB 541 TTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATAAACATTTTACATGACGCTATT 600
QY 603 CAAAGTGTGTGGATTAATTTAGGATCATCCCTTGGTTTAAATAAATGTTGTTCTGCT 662
DB 601 CAAAGTGTGTGGATTAATTTAGGATCATCCCTTGGTTTAAATAAATGTTGTTCTGCT 660

RESULT 7

BD203735 720 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Human nucleic acid sequence originating in ovarian myoma tissue.
ACCESSION BD203735
VERSION BD203735.1 GI:33013505

KEYWORDS

JP 2002511252-A/76.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 720)
AUTHORS Specht, F., Hinzmann, B., Schmitt, A., Pilarsky, C., Dahl, E. and Rosenthal, A.
TITLE Human nucleic acid sequence originating in ovarian myoma tissue
JOURNAL Patent: JP 2002511252-A 76 16-APR-2002;
COMMENT METAGEN GESELLSCHAFT FUER GENOME FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002511252-A/76
PD 16-APR-2002
PF 07-APR-1999 JP 2000543588
PR 09-APR-1998 DE 198 17 557.4
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL
PC C12N15/09, A61K38/00, A61P15/00, A61P35/00, C07K14/82,
PC C07K16/32,
PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/
PC 574,
PC C12N15/00, A61K37/02, C12N5/00
CC Human nucleic acid sequence originating in ovarian myoma CC

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match 99.7%; Score 660; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 5.2e-146;

Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCCGACGAGACCCCTCTCTGACCGCAGCCGCGCCGACCCACCATGGCCACAGTTCA 62

DB 42 CGCCGACGAGACCCCTCTCTGACCGCAGCCGCGCCGACCCACCATGGCCACAGTTCA 101

QY 63 GCAGCTGGAAGGAGATGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAGGA 122

DB 102 GCAGCTGGAAGGAGATGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAGGA 161

QY 123 GCTAGAGTGGGAATAGCTTTTGGAAAAATGGCGCAATGGCCAGCCAGATTGTATCAT 182

DB 162 GCTAGAGTGGGAATAGCTTTTGGAAAAATGGCGCAATGGCCAGCCAGATTGTATCAT 221

QY 183 CACTTGTGATGTTAAACCTCACCATAAACTGAGAGCATTTCAGAACACACAGTT 242

DB 222 CACTTGTGATGTTAAACCTCACCATAAACTGAGAGCATTTCAGAACACACAGTT 281

QY 243 TTCTGTACCTGGGAGAGAGTTTGAAGAAACACAGCTGTAGTGGCAGAAAACTCAGAC 302

DB 282 TTCTGTACCTGGGAGAGAGTTTGAAGAAACACAGCTGTAGTGGCAGAAAACTCAGAC 341

QY 303 TGTCTGCAACTTTACAGATGGTGCTATGTTTACGATACAGGAGTGGGAGGAGAAAG 362

DB 342 TGTCTGCAACTTTACAGATGGTGCTATGTTTACGATACAGGAGTGGGAGGAGAAAG 401

QY 363 CACATAACAGAAATTTGAAGATGGGAAATTTAGTGGTGGAGTGTCATGACAACTGT 422

DB 402 CACATAACAGAAATTTGAAGATGGGAAATTTAGTGGTGGAGTGTCATGACAACTGT 461

QY 423 CACTTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTTGGACAGGA 482

DB 462 CACTTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTTGGACAGGA 521

QY 483 GTTAATTAAGAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTTTCTTCT 542

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603 CAAAGTGTGTTGGATTAATTAGATCATCCCTTTGGTTAATAAATAAATGTTGTGCT 662
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642 CAAAGTGTGTTGGATTAATTAGATCATCCCTTTGGTTAATAAATAAATGTTGTGCT 701

RESULT 8
AX014890
LOCUS
DEFINITION
Sequence 89 from Patent WO9953040.
ACCESSION
AX014890
VERSION
AX014890.1 GI:10041157
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pilarczyk,C.
TITLE
Human nucleic acid sequences from ovarian tumour tissue
JOURNAL
Patent: WO 9953040-A 89 21-OCT-1999;
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GBS FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
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Location/Qualifiers
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/mol_type="unassigned DNA"
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ORIGIN
Query Match 99.7%; Score 660; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 5.2e-146;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCGAGCGCAGACCCCTCTCTGACGCCAGCCCGCCGCCACCCACCATGCGCCACAGTTCA 62
DB 42 CGCGAGCGCAGACCCCTCTCTGACGCCAGCCCGCCGCCACCCACCATGCGCCACAGTTCA 101
QY 63 CGAGCTGGAAGGAAGTGGCGCTGTGTGGACAGCAAGGCTTTGATGATATACATGAAGGA 122
DB 102 CGAGCTGGAAGGAAGTGGCGCTGTGTGGACAGCAAGGCTTTGATGATATACATGAAGGA 161
QY 123 GCTAGAGTGGGAATAGCTTTTGGGAAAATGGCGCAATGGCGAAGCCAGATTTGATCAT 182
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DB 342 TGTCTGCAATTTACAGATGGTGCATTTGTTGATCATCAGGATGGGATGGGAAGGAAG 401
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DB 402 CACAATAACAGAAAATTCGAAGATCGGAAATTTAGTGTGGAGTGTGTCATGAACAATCT 461
QY 423 CACCTGTACTCGGATCTATGAAAAGTAGAATAAATAATCCATCATCATCTTTGGACAGGA 482
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QY 603 CAAAGTGTGTTGGATTAATTAGATCATCCCTTTGGTTAATAAATAAATGTTGTGCT 662
DB 642 CAAAGTGTGTTGGATTAATTAGATCATCCCTTTGGTTAATAAATAAATGTTGTGCT 701

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RESULT 9
BC070303
LOCUS
DEFINITION
Homo sapiens fatty acid binding protein 5 (psoriasis-associated),
mRNA (cDNA clone MGC:88301 IMAGE:6496304), complete cds.
ACCESSION
BC070303
VERSION
BC070303.1 GI:47125411
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 706)
AUTHORS
Straussberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Loquellano,N.A., Peters,G.J.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shewchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

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TITLE
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED
12477932
REFERENCE
2 (bases 1 to 706)
AUTHORS
Straussberg,R.
DIRECT SUBMISSION
Submitted (10-MAY-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

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Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAL Plate: 57 Row: j Column: 10

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557580.

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Best Local Similarity 100.0%; Pred. No. 1.5e-145;
Matches 658; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 255 TTCTTGTACCTGGGAGAGAGTTTGAAGAAACACAGCTGATGGCAGAAAACCTCAGAC 314
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DB 315 TGTCTGCACTTTACAGATGGTGCATTTGTTACGATCAGGAGTGGGATGGGAAGAAAG 374
QY 363 CACAATAACAGAAATTCAGAGATGGGAATTTAGTGGTGGAGTGTCTATGACAACTGT 422
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RESULT 10
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LOCUS
DEFINITION
Sequence 143 from Patent WO0177389.
AX281734
ACCESSION
AX281734.1 GI:16608985
VERSION
KEYWORDS
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Shiffman,D., Somogyi,R., Lawn,R., Seilhamer,J.J., Porter,G.J.,
Mikita,T. and Tai,J.
TITLE
Genes expressed in foam cell differentiation
JOURNAL
Patent: WO 0177389-A 143 18-OCT-2001;
Incyte Genomics, Inc. (US)
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Best Local Similarity 99.8%; Pred. No. 2.1e-143;
Matches 660; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 3 CGCCGACGAGACCCCTCTCTGACCGCAGCCGCCGCGCACCCACCATGCCACAGTTTC 61
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RESULT 11
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DEFINITION Sequence 15640 from Patent WO02069579.
ACCESSION CQ729706
VERSION CQ729706.1 GI:42301523
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
TITLE Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humaneons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15640 06-SEP-2002;
PE Corporation (NV) (US)
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Best Local Similarity 100.0%; Pred. No. 1.9e-142; Indels 0; Gaps 0;
Matches 645; Conservative 0; Mismatches 0;

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sequence.
ACCESSION AP000640
VERSION AP000640.5 GI:28189503
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TITLE Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
JOURNAL Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
REFERENCE Published Only in Database (1999)
2 (bases 1 to 156734)
AUTHORS Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
DIRECT Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
SUBMISSION Direct Submission
JOURNAL Submitted (28-OCT-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan, 305-8565, Japan
(E-mail: hattori@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT On Jan 31, 2003 this sequence version replaced gi:17425221.
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Best Local Similarity 100.0%; Pred. No. 1.7e-142; Indels 0; Gaps 0;
Matches 645; Conservative 0; Mismatches 0;

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DEFINITION Homo sapiens chromosome 11 clone RP11-568F15 map 11, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
ACCESSION AC021809
VERSION AC021809.5 GI:14030015
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-568F15
Unpublished
REFERENCE 1 (bases 1 to 195396)
2 (bases 1 to 195396)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Becker,R., Beckwith,T., Bieda,P.,
Boguslavsky,L., Boucknight,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Collangelo,M., Collins,S., Collamore,A., Cooke,P.,
DeArrellano,K., Dewar,K., Domino,M., Doyle,M., Feneator,J.,
Ferrelita,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lebecky,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,

Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,N.
Direct Submission
Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 13, 2001 this sequence version replaced gi:12061487.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: I5111
Center clone name: 568_F15
----- Summary Statistics
Sequencing vector: M13; M7815; 45% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 194127 bases at least Q40
Consensus quality: 194644 bases at least Q30
Consensus quality: 194869 bases at least Q20
Insert size: 191000; agarose-fp
Insert size: 195096; sum-of-contigs
Quality coverage: 11.4 in Q20 bases; agarose-fp
Quality coverage: 11.1 in Q20.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 48151: contig of 48151 bp in length
* 48152 48251: gap of 100 bp
* 48252 126200: contig of 77949 bp in length
* 126201 126300: gap of 100 bp
* 126301 162491: contig of 36191 bp in length
* 162492 162591: gap of 100 bp
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* Location/Qualifiers
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ORIGIN
Query Match 97.4%; Score 645; DB 2; Length 195396;
Best Local Similarity 100.0%; Pred. No. 1.7e-142; Indels 0;
Matches 645; Conservative 0; Mismatches 0; Gaps 0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 15:11:38 ; Search time 251.715 Seconds
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8314.170 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 1279
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	73.4	5.7	354	3	US-09-643-597-143
5	73.4	5.7	354	4	US-09-480-884A-143
6	73.4	5.7	354	4	US-09-542-615A-143
7	73.4	5.7	354	4	US-09-606-421B-143
8	73.4	5.7	354	4	US-09-221-107-143
9	73.4	5.7	354	4	US-09-466-396A-143
10	73.4	5.7	354	4	US-09-476-496A-143
11	73.4	5.7	354	4	US-09-630-940B-143
12	73.4	5.7	354	4	US-09-285-479-143
13	70	5.5	620	4	US-09-949-016-1540
14	65.6	5.1	601	4	US-09-949-016-42044
15	65.6	5.1	8597	4	US-09-949-016-12945
16	61.2	4.8	9739	4	US-09-949-016-12131
17	61.2	4.8	9739	4	US-09-949-016-13281
18	60.8	4.8	463	3	US-09-513-999C-14348
19	59.8	4.7	731	3	US-09-043-646-1
20	59.8	4.7	731	4	US-09-971-187-1
21	59.8	4.7	1022	4	US-09-949-016-1203
22	56.6	4.4	7218	1	US-08-232-463-14
23	56.2	4.4	493	4	US-09-513-999C-3851
24	56.2	4.4	606	4	US-09-513-999C-3961
25	56.2	4.4	2149	4	US-09-949-016-1539
26	56.2	4.4	2150	4	US-09-949-016-389
27	55.2	4.3	429	4	US-09-799-451-387

Query Match 9.8%; Score 125; DB 1; Length 408;
Best Local Similarity 78.8%; Pred. No. 4.1e-30;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189

28	54.6	4.3	611	4	US-09-621-976-12879	Sequence 12879, A
29	50.6	4.0	505	4	US-09-621-976-15639	Sequence 15639, A
30	47.8	3.7	1717	1	US-08-468-709B-6	Sequence 6, Appli
31	47.8	3.7	1717	2	PCT-US93-03936-6	Sequence 6, Appli
32	47.8	3.7	1717	5	US-09-404-879A-333	Sequence 333, App
33	44.6	3.5	384	3	US-09-667-857-333	Sequence 333, App
34	44.6	3.5	384	4	US-09-702-705-61	Sequence 61, Appl
35	44.6	3.5	466	4	US-09-736-457-61	Sequence 61, Appl
36	44.6	3.5	466	4	US-09-614-124B-61	Sequence 61, Appl
37	44.6	3.5	466	4	US-09-671-325-61	Sequence 61, Appl
38	44.6	3.5	466	4	US-09-589-184-61	Sequence 61, Appl
39	44.6	3.5	466	4	US-09-658-824-61	Sequence 61, Appl
40	44.6	3.5	924	1	US-08-468-709B-1	Sequence 1, Appli
41	44.6	3.5	924	2	US-08-241-664B-1	Sequence 1, Appli
42	44.6	3.5	924	4	US-09-640-173-174	Sequence 174, App
43	44.6	3.5	924	4	US-09-713-550-174	Sequence 174, App
44	44.6	3.5	924	4	US-09-825-294-174	Sequence 174, App
45	44.6	3.5	924	4		

ALIGNMENTS

RESULT 1
US-08-446-600A-3

; Sequence 3, Application US/08446600A
; Patent No. 5719126

; GENERAL INFORMATION:

; APPLICANT: No. 5719126dlund, James J. and Farcoqui, Jamal Z.

; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING THE

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Frost & Jacobs

; STREET: 2500 PNC Center, 201 East Fifth St.

; CITY: Cincinnati

; STATE: OH

; COUNTRY: USA

; ZIP: 45202-4182

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,600A

; FILING DATE: 24 May 1995

; CLASSIFICATION: 514

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 07/980,513

; FILING DATE: 24 No. 5719126member 1992

; APPLICATION NUMBER: PCT/US93/11139

; FILING DATE: 16 No. 5719126member 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Ann G. Robinson

; REGISTRATION NUMBER: 39,820

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (513) 651-6128

; TELEFAX: (513) 651-6981

; TELEX: 21-4396 F&J Cln

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 408 bases

; TYPE: nucleic acid

; STRANDEDNESS: Single

; TOPOLOGY: Unknown

US-08-446-600A-3

Db 78 AGAGTGGGAATAGCTTTGCGAATAATGGCGCAATGGCCAGCCAGATGTGTATCATCAC 137
QY 190 GTGTGATGGCAACAACATCACCGGTCAAAACCCGAGAGCAGTGAAGACGACTGTGTCTC 249
Db 138 TTGTGATGTAATAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACAGTTTTTC 197
QY 250 TTGTAACCTGGGAGAGAGTGTGTAACACGACACTGATGCAGAAAACTGAGGTCTAG 309
Db 198 TTGTACCTGGGAGAGAGTGTGTAAGAAACCCACGCTGTATGCAGAAAACTCAGACTGT 257
QY 310 CTACAACAT 318
Db 258 CTGCAACTT 266

RESULT 2
US-09-949-016-16651/c
; Sequence 16651, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16651
; LENGTH: 45762
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16651

Query Match
Best Local Similarity 9.8%; Score 125; DB 4; Length 45762;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 130 AGAGTAGGACTGGCTTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATCAC 189
Db 28038 AGGAGTGGGAATAGCTTTGCGAATAATGGCGCAATGGCCAGCCAGATTTGTATCATCAC 27979
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGTGAAGACGACTGTGTCTC 249
Db 27978 TTGTGATGTAATAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACAGTTTTTC 27919
QY 250 TTGTAACCTGGGAGAGAGTGTGTAAGAAACCCAGCTGATGCAGAAAACTGAGGTCTAG 309
Db 27918 TTGTACCTGGGAGAGAGTGTGTAAGAAACCCAGCTGATGCAGAAAACTCAGACTGT 27859
QY 310 CTACAACAT 318
Db 27858 CTGCAACTT 27850

RESULT 3
US-09-949-016-13282
; Sequence 13282, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13282
; LENGTH: 8524
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13282

Query Match
Best Local Similarity 6.0%; Score 76.4; DB 4; Length 8524;
Matches 125; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 117 TTTCATATACCCACAGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAG 176
Db 4602 TTTTCTTAAGTGTAGGAGTGGCTTTGCCACCAAGAAAGTGGCTGGCATGGCCAAACCTA 4661
QY 177 ACTGTATCATTCAGTGTGATGCGCAACAACATCACCGTCAAAACCCGAGAGCAGTGAAGA 236
Db 4662 ACATGATCATCAGTGTGAATGGGATGTGATCACCATTAATAATCTGAAAGTACCTTTAAA 4721
QY 237 CGACTGTGTCTCTTGTAACTGGGAGAGAGTGTGATGMAACGACAGCTGATGCAGAA 296
Db 4722 ATACTGAGATTTCTTTCATCTAGGCGCCAGGAATTTGACAAAGTCACTGCAGATGACAGA 4781
QY 297 AAACCTGAGTCACTGCTACCAACATACCTG 322
Db 4782 AAGTCAAGGTGAGAAATAAGGAGTG 4807

RESULT 4
US-09-643-597-143
; Sequence 143, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Lijun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-143

Query Match
Best Local Similarity 5.7%; Score 73.4; DB 3; Length 354;
Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY 630 CAGACGGTCTGCACCTTCCAGACCGTGCCTGTCCAGCCAGCAATGGGACGGGAAG 689
Db 22 CAGACTGTCTGCAACTTTACAGATGGTGCATTTGTTTACAGATCAGAGTGGGATGGGAAG 81
QY 690 GAGAGCAGGATAACAAGAAACTGAAGGATGGGAAGATGATCGTGTGTGAGCATCA 744

Db 82 GAAAGCACATACACAGAAATTGAAAGATGGGAATTTAGTGGTGGAGTGTGTCA 136

RESULT 5

US-09-480-884A-143
; Sequence 143, Application US/09480884A

; Patent No. 6482597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C6

; CURRENT APPLICATION NUMBER: US/09/480,884A

; CURRENT FILING DATE: 2001-08-27

; NUMBER OF SEQ ID NOS: 330

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 143

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-480-884A-143

Query Match 5.7%; Score 73.4; DB 4; Length 354;

Best Local Similarity 77.4%; Pred. No. 2.7e-13;

Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGCGGTGCCCTGTCAGACACGCAATGGGACGGGAAG 689

Db 22 CAGACTGTCTGCAACTTTACAGATGGTGCAATTGTTTCAGCATCAGGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATACACAGAACTGAGGATGGGAAGATGATCTGTTGAGCATCA 744

Db 82 GAAAGCACATACACAGAAATTGAAAGATGGGAATTTAGTGGTGGAGTGTGTCA 136

RESULT 6

US-09-542-615A-143

; Sequence 143, Application US/09542615A

; Patent No. 6518256

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C8

; CURRENT APPLICATION NUMBER: US/09/542,615A

; CURRENT FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 143

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-542-615A-143

Query Match 5.7%; Score 73.4; DB 4; Length 354;

Best Local Similarity 77.4%; Pred. No. 2.7e-13;

Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGCGGTGCCCTGTCAGACACGCAATGGGACGGGAAG 689

Db 22 CAGACTGTCTGCAACTTTACAGATGGTGCAATTGTTTCAGCATCAGGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATACACAGAACTGAGGATGGGAAGATGATCTGTTGAGCATCA 744

Db 82 GAAAGCACATACACAGAAATTGAAAGATGGGAATTTAGTGGTGGAGTGTGTCA 136

RESULT 7

US-09-606-421B-143

; Sequence 143, Application US/09606421B

; Patent No. 6531315

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606,421B

; CURRENT FILING DATE: 2000-06-28

; NUMBER OF SEQ ID NOS: 358

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 143

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-606-421B-143

Query Match 5.7%; Score 73.4; DB 4; Length 354;

Best Local Similarity 77.4%; Pred. No. 2.7e-13;

Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGCGGTGCCCTGTCAGACACGCAATGGGACGGGAAG 689

Db 22 CAGACTGTCTGCAACTTTACAGATGGTGCAATTGTTTCAGCATCAGGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATACACAGAACTGAGGATGGGAAGATGATCTGTTGAGCATCA 744

Db 82 GAAAGCACATACACAGAAATTGAAAGATGGGAATTTAGTGGTGGAGTGTGTCA 136

RESULT 8

US-09-221-107-143

; Sequence 143, Application US/09221107

; Patent No. 6660838

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER

; FILE REFERENCE: 210121.455C2

; CURRENT APPLICATION NUMBER: US/09/221,107

; CURRENT FILING DATE: 1998-12-22

; NUMBER OF SEQ ID NOS: 161

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 143

; LENGTH: 354

; TYPE: DNA

; ORGANISM: Human

US-09-221-107-143

Query Match 5.7%; Score 73.4; DB 4; Length 354;

Best Local Similarity 77.4%; Pred. No. 2.7e-13;

Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGCGGTGCCCTGTCAGACACGCAATGGGACGGGAAG 689

Db 22 CAGACTGTCTGCAACTTTACAGATGGTGCAATTGTTTCAGCATCAGGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATACACAGAACTGAGGATGGGAAGATGATCTGTTGAGCATCA 744

Db 82 GAAAGCACATACACAGAAATTGAAAGATGGGAATTTAGTGGTGGAGTGTGTCA 136

```
RESULT 9
US-09-466-396A-143
; Sequence 143, Application US/09466396A
; Patent No. 6696247
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-466-396A-143

Query Match          5.7%; Score 73.4; DB 4; Length 354;
Best Local Similarity 77.4%; Pred. No. 2.7e-13;
Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGACGGTGCCTGGTCCAGCACCAGCAATGGGACGGGAAG 689
Db 22 CAGACTGTCTGCACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATTAACAAGAAAACCTGAAGGATGGGAAGATGATCGTGGTGAGCATCA 744
Db 82 GAAAGCACATAACAAGAAAATTGAAAGATGGGAAAATTAGTGGTGGAGTGTGTCA 136

RESULT 10
US-09-476-496A-143
; Sequence 143, Application US/09476496A
; Patent No. 6706262
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: LUNG CANCER
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476,496A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-476-496A-143

Query Match          5.7%; Score 73.4; DB 4; Length 354;
Best Local Similarity 77.4%; Pred. No. 2.7e-13;
Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGACGGTGCCTGGTCCAGCACCAGCAATGGGACGGGAAG 689
Db 22 CAGACTGTCTGCACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATTAACAAGAAAACCTGAAGGATGGGAAGATGATCGTGGTGAGCATCA 744
Db 82 GAAAGCACATAACAAGAAAATTGAAAGATGGGAAAATTAGTGGTGGAGTGTGTCA 136

RESULT 11
US-09-630-940B-143
; Sequence 143, Application US/09630940B
; Patent No. 6737514
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-630-940B-143

Query Match          5.7%; Score 73.4; DB 4; Length 354;
Best Local Similarity 77.4%; Pred. No. 2.7e-13;
Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGACGGTGCCTGGTCCAGCACCAGCAATGGGACGGGAAG 689
Db 22 CAGACTGTCTGCACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATTAACAAGAAAACCTGAAGGATGGGAAGATGATCGTGGTGAGCATCA 744
Db 82 GAAAGCACATAACAAGAAAATTGAAAGATGGGAAAATTAGTGGTGGAGTGTGTCA 136

RESULT 12
US-09-285-479-143
; Sequence 143, Application US/09285479
; Patent No. 6821518
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; TITLE OF INVENTION: LUNG CANCER
; FILE REFERENCE: 210121.455C3
; CURRENT APPLICATION NUMBER: US/09/285,479
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-285-479-143

Query Match          5.7%; Score 73.4; DB 4; Length 354;
Best Local Similarity 77.4%; Pred. No. 2.7e-13;
Matches 89; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 630 CAGACGGTCTGCACCTTCCAAAGACGGTGCCTGGTCCAGCACCAGCAATGGGACGGGAAG 689
Db 22 CAGACTGTCTGCACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGATGGGATGGGAAG 81

QY 690 GAGAGCAGCATTAACAAGAAAACCTGAAGGATGGGAAGATGATCGTGGTGAGCATCA 744
Db 82 GAAAGCACATAACAAGAAAATTGAAAGATGGGAAAATTAGTGGTGGAGTGTGTCA 136

RESULT 13
US-09-949-016-1540
; Sequence 1540, Application US/09949016
```

Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1540
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1540

Query Match 5.1%; Score 70; DB 4; Length 620;
Best Local Similarity 60.5%; Pred. No. 5.2e-12; Indels 0; Gaps 0;
Matches 115; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
DB 119 AGGAGTGGGCTTTGCCACAGGAAGTGGCTGGCCAACTTAACATGATCATCAG 178
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 179 TGTGAATGGGGATGTGATCACCATTAAATCTGAAAGTACCTTTAAATACTGAGATTTC 238
QY 250 TTGTACCTGGGAGAGAACTTTGATCAACAGCAGCTGTGGCAGAAAACCTGAGCTCAG 309
DB 239 CTTCATCTGGGCCAGGAATTTGACGAAGTCACTGCAGATGACAGGAAGTCAAGAGCAC 298
QY 310 CTACAACATA 319
DB 299 CATAACCTTA 308

RESULT 14
US-09-949-016-42044
; Sequence 42044, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42044
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-42044

Query Match 5.1%; Score 65.6; DB 4; Length 601;
Best Local Similarity 58.0%; Pred. No. 1.4e-10;
Matches 116; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189

DB 362 AGCGTGGGCTTTGCCACTAGGCGAGTGGGAAATGTGACCAACCGTAATTATTCAG 421
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 422 TCAGAGAGGAGACAAAGTGGTCAATCAGGACTCTCAGCACATTCAGAGACGAGATTAG 481
QY 250 TTGTAACTGGGAGAGAACTTTGATGAAAACGACAGCTGTGGCAGAAAAAAGCTGAGTTCAG 309
DB 482 TTTCCAGCTGGGAGAGAGTTTGTATGAAACCACTGCAGATGATAGAAACTGTGAAGGTGAG 541
QY 310 CTACAACATACTGTGAAGCG 329
DB 542 AAACCTGCTTCTTCTTCAGAG 561

RESULT 15
US-09-949-016-12945
; Sequence 12945, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12945
; LENGTH: 8597
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12945

Query Match 5.1%; Score 65.6; DB 4; Length 8597;
Best Local Similarity 58.0%; Pred. No. 8.8e-10;
Matches 116; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
DB 2815 AGCGTGGGCTTTGCCACTAGGCGAGTGGGAAATGTGACCAACCGTAATTATTCAG 2874
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 2875 TCAGAGAGGAGACAAAGTGGTCAATCAGGACTCTCAGCACATTCAGAGACGAGATTAG 2934
QY 250 TTGTAACTGGGAGAGAACTTTGATGAAAACGACAGCTGTGGCAGAAAAAAGCTGAGTTCAG 309
DB 2935 TTTCCAGCTGGGAGAGAGTTTGTATGAAACCACTGCAGATGATAGAAACTGTGAAGGTGAG 2994
QY 310 CTACAACATACTGTGAAGCG 329
DB 2995 AAACCTGCTTCTTCTTCAGAG 3014

Search completed: July 12, 2005, 18:08:06
Job time : 253.715 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 15:11:34 ; Search time 807.859 Seconds
(without alignments)
9372.119 Million cell updates/sec

Title: US-09-788-074-2
Perfect score: 1279
Sequence: 1 aatgggagcaacatgctagc.....tctatgagaagtgcataga 1279

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_16Dec04:*
- 1: Geneseqn1980s:*
 - 2: Geneseqn1990s:*
 - 3: Geneseqn2000s:*
 - 4: Geneseqn2001as:*
 - 5: Geneseqn2001bs:*
 - 6: Geneseqn2002as:*
 - 7: Geneseqn2002bs:*
 - 8: Geneseqn2003as:*
 - 9: Geneseqn2003bs:*
 - 10: Geneseqn2003cs:*
 - 11: Geneseqn2003ds:*
 - 12: Geneseqn2004as:*
 - 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1279	100.0	1279	4	AAS13246 Mouse DNA
2	284	22.2	3247	9	ACC42875 Adenosine
3	176.6	13.8	933	12	ADJ75985 Marker ge
4	175.6	13.7	537	12	ACH72029 Human gen
5	165	12.9	1623	6	ABSG6521 Mouse Fab
6	144.2	11.3	643	6	ABK71797 Human dit
7	144.2	11.3	695	10	ADF30639 Rat angio
8	144.2	11.3	704	10	ADP30635 Rat angio
9	144.2	11.3	704	10	ADP72791 Renal tox
10	142.6	11.1	664	10	ADB53766 Primary r
11	142.6	11.1	664	10	ADP30637 Rat angio
12	129.8	10.1	335	6	ABL92950 Rat metas
13	129.8	10.1	335	12	ADN07741 Human mam
14	125	9.8	408	2	AAQ66842 Melanogen
15	125	9.8	461	6	ABK53980 Human hea
16	125	9.8	479	9	ACH38376 Human end
17	125	9.8	494	9	ACH35892 Human end
18	125	9.8	519	6	ABK53994 Human hea
19	125	9.8	606	6	ABK53952 Human hea
20	125	9.8	612	10	ADK11762 Breast ca

21	125	9.8	615	6	ABK53828 Human hea
22	125	9.8	662	4	AAS13247 Human DNA
23	125	9.8	662	6	ABV77978 Hypoxia-r
24	125	9.8	662	10	ADB75278 Prostate
25	125	9.8	662	10	ADH28827 Human chr
26	125	9.8	662	12	ADJ75120 Marker ge
27	125	9.8	662	12	ADN03852 Antipeori
28	125	9.8	662	12	ADO19263 Human PRO
29	125	9.8	662	12	ADP13321 Renal cel
30	125	9.8	662	13	ADR24747 Breast ca
31	125	9.8	662	13	ACN38822 Tumour-as
32	125	9.8	662	13	ADP54337 Human PRO
33	125	9.8	662	13	ADR52981 Drug ther
34	125	9.8	662	13	ADP25373 PRO polyo
35	125	9.8	662	13	ADR99018 Fatty aci
36	125	9.8	662	13	ADR66234 Human pro
37	125	9.8	662	13	ADR66576 Human pro
38	125	9.8	720	2	AZ77538 Human ova
39	125	9.8	1071	10	ADB47413 Human CDN
40	125	9.8	1071	11	ADM86791 Human DNA
41	125	9.8	1072	6	AAS94888 Human DNA
42	124	9.7	331	6	ABK53860 Human hea
43	123.4	9.6	627	9	AAD57420 Human FAB
44	121.8	9.5	540	9	AAD57419 Human fat
45	121.8	9.5	660	12	ADQ86530 Human tum

ALIGNMENTS

RESULT 1
AAS13246
ID AAS13246 standard; DNA; 1279 BP.
XX
AC AAS13246;
XX

DT 18-DEC-2001 (first entry)
XX

DE Mouse DNA encoding keratinocyte fatty acid binding protein, Mall.
KW Mouse; Mal 1; keratinocyte fatty acid binding protein; ds; anorectic;
KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
KW dyslipidaemia; atherosclerosis; antisense therapy.
XX

OS Mus musculus.

EH Key
FT CDS Location/Qualifiers
132..1279

FT exon /product= "Mal 1"

FT /tag= a

FT /tag= b

FT /tag= c

FT /tag= d

FT /tag= e

FT /tag= f

FT /tag= g

FT /tag= h

FT /tag= i

FT /tag= j

FT /tag= k

FT /tag= l

FT /tag= m

FT /tag= n

FT /tag= o

FT /tag= p

FT /tag= q

FT /tag= r

FT /tag= s

FT /tag= t

FT /tag= u

FT /tag= v

FT /tag= w

FT /tag= x

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FT /tag= z

FT /tag= AA

FT /tag= AB

FT /tag= AC

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FT /tag= AE

FT /tag= AF

FT /tag= AG

FT /tag= AH

FT /tag= AI

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FT /tag= AK

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FT /tag= AM

FT /tag= AN

FT /tag= AO

FT /tag= AP

FT /tag= AQ

FT /tag= AR

FT /tag= AS

FT /tag= AT

FT /tag= AU

FT /tag= AV

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FT /tag= AX

FT /tag= AY

FT /tag= AZ

FT /tag= BA

FT /tag= BB

FT /tag= BC

FT /tag= BD

FT /tag= BE

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FT /tag= BG

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FT /tag= BJ

FT /tag= BK

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FT /tag= BO

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FT /tag= BQ

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FT /tag= BV

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FT /tag= BX

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FT /tag= BZ

FT /tag= CA

FT /tag= CB

FT /tag= CC

FT /tag= CD

FT /tag= CE

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FT /tag= GM

FT /tag= GN

FT /tag= GO

FT /tag= GP

FT /tag= GQ

FT /tag= GR

FT /tag= GS

FT /tag= GT

FT /tag= GU

FT /tag= GV

FT /tag= GW

FT /tag= GX

FT /tag= GY

PF 16-FEB-2001; 2001WO-US005019.
 XX
 PR 17-FEB-2000; 2000US-0183106P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Hotamisligil GS;
 XX
 PI
 XX
 DR WPI: 2001-570550/64.
 XX P-PSDB; AAU08673.
 XX
 PT Reducing the level of circulating free fatty acids in a mammal, useful
 PT for treating or preventing obesity, diabetes, dyslipidemia or
 PT atherosclerosis, by administering a keratinocyte lipid binding protein
 PT inhibitor.
 XX
 XX
 PS Disclosure; Page 2; 27pp; English.
 XX
 PS The invention relates to reducing the level of circulating free fatty
 CC acids in a mammal comprising administering to a mammal a compound that
 CC inhibits expression (e.g. by antisense therapy) of Mall (keratinocyte
 CC fatty acid binding protein) or Mall activity. The method is useful for
 CC reducing the level of circulating free fatty acids in a mammal,
 CC particularly in a mammal that is suffering from or at risk of developing
 CC obesity, diabetes, dyslipidaemia or atherosclerosis. The method is also
 CC useful for diagnosing these diseases. The present sequence encodes Mouse
 CC Mal 1
 XX
 SQ Sequence 1279 BP; 381 A; 242 C; 340 G; 316 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1279; DB 4; Length 1279;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGGAGCAACATGCTAGCTATGCAGTCCGTGAGTGAGTGAGTGACAAAGGCT 60
 DB
 QY 1 AATGGAGCAACATGCTAGCTATGCAGTCCGTGAGTGAGTGAGTGACAAAGGCT 60
 DB
 QY 61 GGCAGTGGGATGAAGAAATGAATCTTGTCTTATCATTTGACAAATACGTCATTTTC 120
 DB
 QY 61 GGCAGTGGGATGAAGAAATGAATCTTGTCTTATCATTTGACAAATACGTCATTTTC 120
 DB
 QY 121 CATACCCACAGGATGAGTGGCTCTTAAAGAGATGGCTGCATGGCCCAAGCCAGACTG 180
 DB
 QY 121 CATACCCACAGGATGAGTGGCTCTTAAAGAGATGGCTGCATGGCCCAAGCCAGACTG 180
 DB
 QY 181 TATCATTACGTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGAGTGAAGACGAC 240
 DB
 QY 181 TATCATTACGTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGAGTGAAGACGAC 240
 DB
 QY 241 TGTGTTCTTGTAACTGGGAGAGAGTTTGTATGAAAGCAGAGCTGATGGCAGAAAC 300
 DB
 QY 241 TGTGTTCTTGTAACTGGGAGAGAGTTTGTATGAAAGCAGAGCTGATGGCAGAAAC 300
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 QY 301 TGAGGTGACGTACACATCTGTGAAGCGACAGAGACTTCTAGATTTACAGATTAATTTG 360
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 QY 301 TGAGGTGACGTACACATCTGTGAAGCGACAGAGACTTCTAGATTTACAGATTAATTTG 360
 DB
 QY 361 CATTAAACATGCTGTACTTACTGCAAGGGCTGACTGAAAAAACTACTTTATGAGTTG 420
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 QY 361 CATTAAACATGCTGTACTTACTGCAAGGGCTGACTGAAAAAACTACTTTATGAGTTG 420
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 QY 421 ACTTTTGTAAATAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCT 480
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 QY 421 ACTTTTGTAAATAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCT 480
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 QY 481 AGATCGAAAGCACATAGTTGTATGTGAACAAATACAGTATGATGGGTGGAGTTTCA 540
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 QY 481 AGATCGAAAGCACATAGTTGTATGTGAACAAATACAGTATGATGGGTGGAGTTTCA 540
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 QY 541 GAGGAAAGCGAAGACTTGTGGAGTGTGTGGGTCTTGGGGTTCCTTCACTTTGGAA 600
 DB
 QY 541 GAGGAAAGCGAAGACTTGTGGAGTGTGTGGGTCTTGGGGTTCCTTCACTTTGGAA 600
 DB

QY 601 GATGATGAACCTAACCTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTGCCC 660
 DB
 QY 601 GATGATGAACCTAACCTACCTGTATTTTTCAGACGGTCTGCACCTTCCAAAGACGGTGCCC 660
 DB
 QY 661 TGGTCCAGCACAGCAATGGGACGGGAGGAGAGACGATAAACAAGAAAACCTGAAGGATG 720
 DB
 QY 661 TGGTCCAGCACAGCAATGGGACGGGAGGAGAGACGATAAACAAGAAAACCTGAAGGATG 720
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 QY 721 GGAAGATGATCGTGTGAGCATCAAAAGCACTGGGACCATGCTGGGATTTGGGCTCGAGCC 780
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 QY 721 GGAAGATGATCGTGTGAGCATCAAAAGCACTGGGACCATGCTGGGATTTGGGCTCGAGCC 780
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 QY 781 ACAGTTGTCAATAACCACTTGGGTCTTAAACAAGAGAGGAAAACCTTAGGAGG 840
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 QY 841 ACAATACCTGAAAATAACAAAGTTAGAAAACGAGAGTCTCATTTCTGAGGAGCCCTTTGG 900
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 QY 841 ACAATACCTGAAAATAACAAAGTTAGAAAACGAGAGTCTCATTTCTGAGGAGCCCTTTGG 900
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 QY 901 GGACGGAGAGTGGATCCAGGATGCTGAGGATGCTGAGGAGCTGAGAGCTGGCAGGC 960
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 QY 901 GGACGGAGAGTGGATCCAGGATGCTGAGGATGCTGAGGAGCTGAGAGCTGGCAGGC 960
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 QY 961 CACCGAGCAGCCCTCTCTGCTGATGATTTAAAGTAAAGGATATTTGCCAAAAACACATG 1020
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 QY 961 CACCGAGCAGCCCTCTCTGCTGATGATTTAAAGTAAAGGATATTTGCCAAAAACACATG 1020
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 QY 1021 AATAATTTAGAGATCATATCCAGTCTTTAGTCTGAGGAGCAAAATATACATATAAAC 1080
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 QY 1021 AATAATTTAGAGATCATATCCAGTCTTTAGTCTGAGGAGCAAAATATACATATAAAC 1080
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 QY 1081 AAAACAGAGCTCTAGTCTTCTGAGTTGATCTGAGATGCTGGTTTCTGTTAGT 1140
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 QY 1081 AAAACAGAGCTCTAGTCTTCTGAGTTGATCTGAGATGCTGGTTTCTGTTAGT 1140
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 QY 1141 TGGTTTACAAGCTTTATAGGATTTGCCCAACAACATGCTCTGAAATGTACAGTTGGCC 1200
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 QY 1141 TGGTTTACAAGCTTTATAGGATTTGCCCAACAACATGCTCTGAAATGTACAGTTGGCC 1200
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 QY 1201 TGAGACTCTATCTTTCTCTCTAGGAGTGTGATGAACAAATGCCACCTGCACTCGGCT 1260
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 QY 1201 TGAGACTCTATCTTTCTCTCTAGGAGTGTGATGAACAAATGCCACCTGCACTCGGCT 1260
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 QY 1261 CTATCAGAAGGTGCAATGA 1279
 DB
 QY 1261 CTATCAGAAGGTGCAATGA 1279
 DB

RESULT 2
 ACC42875
 ID ACC42875 standard; cDNA; 3247 BP.
 XX
 AC ACC42875;
 XX
 DT 01-SEP-2003 (first entry)
 XX
 DE Adenosine triphosphate synthetase-10.89 coding sequence.
 XX
 KW Adenosine triphosphate synthetase-10.89; enzyme; hypertension;
 KW peptic ulcer; nephrotic syndrome; asthma; parkinsonism; gene; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT CDS 1868..2167
 FT /*tag= a
 FT /product= "Adenosine triphosphate synthetase-10.89"
 XX
 PN CN1380393-A.
 XX
 PD 20-NOV-2002.

XX 10-APR-2001; 2001CN-00105888.
XX PF
XX PR
XX 10-APR-2001; 2001CN-00105888.
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX PA
XX PI Mao Y, Xie Y;
XX WPI; 2003-230977/23.
XX DR P-PSDB; ABR56128.
XX PT A polypeptide-adenosine triphosphate synthetase-10.89, encoding
PT polynucleotide, antagonist, and recombinant production, useful for
PT treating hypertension, peptic ulcers, nephrotic syndrome, asthma and
PT parkinsonism.
XX PS Claim 6; Page 26-28; 31pp; Chinese.
XX CC The present invention relates to adenosine triphosphate synthetase-10.89
CC and its coding sequence. The protein is useful for treating hypertension,
CC peptic ulcers, nephrotic syndrome, asthma and parkinsonism
XX SQ Sequence 3247 BP; 1007 A; 549 C; 683 G; 1008 T; 0 U; 0 Other;
Query Match 22.2%; Score 284; DB 9; Length 3247;
Best Local Similarity 59.2%; Pred. No. 5.7e-77;
Matches 720; Conservative 0; Mismatches 425; Indels 71; Gaps 11;
QY 126 CCACAGGAGTAGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCA 185
DB 1839 CTACAGGAGTGGGAATAGCTTTGCGAAATATGGCGCAATGGCCAGCCAGATTGTATCA 1898
QY 186 TTACGTGTGATGCAACAACATCACGGTCAAAACCGAGAGCAGGTGAAGACGACTGTGT 245
DB 1899 TCACCTTGATGGTAAACCTCACCATAAACCTGAGAGCACTTTGAAACCAACACAGT 1958
QY 246 TCTCTTGTAACTGGGAGAGAAGTTTGTATGAAACGACAGCTGATGGCAGAAAAAAGTGGAG 305
DB 1959 TTTCTTGT-CCCTGGGAGAGAAGTTTGAAGAAACCAACAGCTGATGGCAGAAAAAAGTGGAG 2017
QY 306 TCAGCTACACATACATGTCGAGGACAGAGCTTCTAGATTACAGATTAAATTCATTA 365
DB 2018 TCAGTCGTGACATGTTATGAATACAGAAAGCTTCTAGAAATGATAGGCTGTAT---CAAT 2074
QY 366 ACAATGCTGTACTTACTGCAAGGCTGACTGAAAAAAGTCTTTATGAGTTTCTAGATC 425
DB 2075 AACATTTTACTGTTATAGGCAAGAACTTATGAAAGAAAGTTATTTAT-GAATGAAATTT 2133
QY 426 TGATAAATAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATC 485
DB 2134 TGTCAAATTAGCAAAAGTATCAACTTCATCATAGAATTTGGCATCTTTTATAGCTACTAG 2193
QY 486 GAAAGCACATAGTTGTATGTGAACAAATCATGATGATGGGTGAGT-----TCAGAG 541
DB 2194 GTTGAACACCAAACTATTTGTGAATTAATCAATATGAGTTTAAATGAAGTAGACTCAGAA 2253
QY 542 AGGGAAGCGGAAGACTTGTGTGAGT-----GCTGGGTCTGGGGTCTCTTCACATT 595
DB 2254 AGGAGAGGTGAACAAATGTTGATTAAAGAGTTATGATCATGGAAGAACTCTTGTAAATG 2313
QY 596 TGAAGATGATGAATCACTACCTGTATTTTTTGCAGAGGTTGTGACCTTCCAGACGG 655
DB 2314 TACTTGGAAAGATTAAACCGTTTACTTTGTTTTTGCAGAGCTGTCTGCAACTTTACAGATGG 2373
QY 656 TGGCCTGGTCCAGCACCAAGCAATGGGACGGGAAGGAGACGATTAACAAAGAAACTGAA 715
DB 2374 TGCATTGGTTTCAGCATCAGAGTGGGATGGGAAGGAAAGCAAAATACCAAGAAATTTGAA 2433
QY 716 GATGGGAAGATGATCGTGTGAGCATCAAGCACTGGCACCACCTGCTGGGATTTGGSCCTG 775
DB 2434 AGATGGAAATTAGTGGTGAAGTGTCAACTGCTGTCTCAGTCAGCTTCTTGTGTG 2493

QY 776 CAGCCACAGTTGTCTATAACCACTTCCGGGTCAATTGGTTCTTTTAAACAAGAGAAACTTAA 835
DB 2494 CATTCATAGTTCACATAACTGTTCTATATCATGATCAIT-----AACAGAACTCAGTTTG 2549
QY 836 GGAGGACATACTGAAAAATAACAAGTTAGAAACGAGAGTCCCTCATTTGCTGAGCGAGCCCT 895
DB 2550 GAAGAAAAAAGCAAAATAACAAGTTAAATTAATACTAGAACACTAATTTATTAAAGAAATCCT 2609
QY 896 TGTGGGACGGAAGTGTATGGG-----ATCCCAGGATGTGGCTGACGACGAGCCTG---- 947
DB 2610 AGTGGAGATAGAGAAGTGCATGACATAGGAGAGGATTTGGCTGGAGTTGGGGGGAGTTTC 2669
QY 948 -----AGAGCTGCAGGCCACCGAGCAGCCCTCTCTCTGGT 982
DB 2670 TTGCTTTTGTGCCACGTCAAGTGAATCTTGGCAAGCCCAAACTGCACACATTTTTC 2729
QY 983 ACATGATTTAAAGTAAGGATATTTGCCAAAAACACATGAATATTTTAGAGATCATATCCA 1042
DB 2730 TATATCTTTAAATAAGGAATATTTGCCATAACCAAAAGAAATAAGATATATTCAACACA 2789
QY 1043 GTGCTTTTACTCTGCAGGGCAGCAAAATATATACATATAAACAACAGCAGCTCTTAGGTCTT- 1101
DB 2790 TTAGTTTTCTGTAAACATGTCATATTTATAAGCAAAAAACACAGCTTCTGGCTTCTCTCAA 2849
QY 1102 CTTGAGTTTGAATCTGAGATGTGGTTTTTCTGTAGGTGGTTTACAGGGTTTATAGGA 1161
DB 2850 CCGCTGAATTTCTGAAAGAAATTTTCTCCATCTATGAAGTAGATTACGTGATTTTCGTGGGA 2909
QY 1162 TTCTGCC-----ACAACACATGCTCTGAAATGTACAGTTGCGCTGAGACTC 1208
DB 2910 CTTTGATTTCTAATGTTTAAATACCACTGCTCTGGAATCTAAGGCTAACCTAACTCTT 2969
QY 1209 T-----ATCTTTTCTCTCTAGGAGTGTGTATGAACAATGCCACCTGCACCTCGGCTCTA 1263
DB 2970 TTAATATCTTCTCTCTAGGAGTGTGTATGAACAATGTCACCTGTACTCGGATCTA 3029
QY 1264 TGAGAAGGTGCAATGA 1279
DB 3030 TGAAGAAAGTAGAATAA 3045
RESULT 3
ADJ75985
ID ADJ75985 standard; DNA; 933 BP.
XX AC ADJ75985;
XX DT 20-MAY-2004 (first entry)
XX DE Marker gene SEQ ID NO:1237.
XX KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker gene; gene; ds.
XX OS Mus musculus.
XX PN EP1394274-A2.
XX PD 03-MAR-2004.
XX PF 04-AUG-2003; 2003EP-00254857.
XX PR 06-AUG-2002; 2002JP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX PA (GENO-) GENOX RES INC.
XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuha K;
XX WPI; 2004-193155/19.
XX DR
XX PT Testing for bronchial asthma or chronic obstructive pulmonary disease by

QY 246 TCTCTTGTAACTGGGAGAGAACTTTGATGAACAGCAGCTGATGGCAGAAAACTGAGG 305
 DB 218 TTTCTTTGTACCTCGGAGAGAACTTTGAAGAAACACAGCTGATGGCAGAAAACTCAGG 277
 QY 306 TCAGCTACAACTACTGTGAAGCGACAGAGAGCTTCTAGATTATACAGATTAAATTCGATT 365
 DB 278 TCAGTCGTGACATGTTATGAATATCAGAGAAGCTTCTAGAAATGATAGCTGTAT---CAAT 334
 QY 366 ACAATCTCTGTACTTACTGTCACAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTT 425
 DB 335 AACATTTTACTGTTTATAGCAAGAACTTAATGAAAAAGTTATTTAT-GAATTGAATTT 393
 QY 426 TGAATAATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCTAGATC 485
 DB 394 TGTCAAAATTAGCAAAAGTATCACTTCATCATAGAAATTCGCATCTTTTATAGTACTAG 453
 QY 486 GAAAGCACATAGTCTGTTGTTGTAACAAATCAGTATGATGGGTGAGT 535
 DB 454 GTTGAACACACAACTATTGTGAAATTAATCAATATGTTGGTTAATGAAGT 503

RESULT 5

AB565621
 ID ABS65621 standard; DNA; 1623 BP.

AC ABS65621;

DT 15-NOV-2002 (first entry)

DE Mouse Fab gene (EMBL No. fabe_mouse) exon 1.

KW Mouse; vertebrate; anorexia/anorexia genotype; anx/anx;
 KW control of food intake; feed; body weight; human; weight gain;
 KW ANKT protein; nucleolar protein; proliferating cell; anorectic;
 KW chromosome 2; gene; ds.

OS Mus musculus.

PN WO200262835-A1.

PD 15-AUG-2002.

PF 08-FEB-2002; 2002WO-S500022.

PR 08-FEB-2001; 2001US-00778844.

PA (APPE-) APPETITE CONTROL AB.

PI Johansen J, Schalling M;

PN WPI; 2002-657520/70.

PT New nucleic acid molecule encoding a polypeptide capable of at least
 PT partially complementing the phenotype of an animal having the anx/anx
 PT genotype, useful for controlling and regulating weight gain and food
 PT intake in humans.

PS Disclosure; Fig 11; 314pp; English.

CC The present invention relates to an isolated nucleic acid molecule
 CC comprising a nucleotide sequence derived from a vertebrate animal (e.g.
 CC mouse), and encodes a polypeptide capable of at least partially
 CC complementing the phenotype of an animal having the anorexia/anorexia
 CC (anx/anx) genotype. The nucleic acid molecule and the polypeptide encoded
 CC by the nucleotide sequence is useful for controlling food or feed intake,
 CC or body weight in animals including humans. The polynucleotide and
 CC polypeptide sequences of the invention are useful for regulating and
 CC controlling weight gain and food intake in animals particularly humans.
 CC The polypeptide sequences are also useful for generating monoclonal or
 CC polyclonal antibodies. The antibodies are useful for diagnostic and
 CC therapeutic purposes. These antibodies can be used in an immunoassay for
 CC identification or detection of the polypeptides. The polynucleotide

CC sequences are useful for recombinant production of large quantities of
 CC the receptor, for further studies into the mechanism of regulation of
 CC food intake and/or body weight and for obtaining agonists and
 CC antagonists. ABS6557-ABS65762 represent mouse gene sequences relating to
 CC the present invention. The gene sequences are located on mouse chromosome
 CC 2

SQ Sequence 1623 BP; 575 A; 332 C; 371 G; 345 T; 0 U; 0 Other;

Query Match 12.9%; Score 165; DB 6; Length 1623;
 Best Local Similarity 92.1%; Pred. No. 5e-40;
 Matches 174; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 130 AGAGTAGAGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
 DB 612 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 671
 QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCAGAGACAGTGAACGACCTGTGTTCTC 249
 DB 672 TTGTGATGGCAACAACATCACCGTCAAAACCCGTGACGACAGTGAACGACCTGTGTTCTC 731
 QY 250 TTGTAACTCTGGGAGAGAGCTTTGATGAAACGACAGCTGATGGCAGAAAACTGAGTCTAG 309
 DB 732 TTGTACCTCTGGGAGAGAGCTTTGATGAAACGACAGCTGATGGCAGAAAACTGAGCGGT 791
 QY 310 CTACAAACAT 318
 DB 792 CTGCACCTT 800

RESULT 6

ABK71797

ID ABK71797 standard; cDNA; 643 BP.

AC ABK71797;

DT 30-JUL-2002 (first entry)

DE Human dithp polynucleotide #263.

KW Human; dithp; diagnostic and therapeutic polynucleotide; gene; ss; bone;
 KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;
 KW inflammatory disorder; viral infection; bacterial infection; seizure;
 KW fungal infection; parasitic infections; developmental disorder; breast;
 KW endocrine disorder; metabolic disorder; neurological disorder; cervix;
 KW gastrointestinal disorder; transport disorder; gene therapy; kidney;
 KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;
 KW skin; testis; thymus.

OS Homo sapiens.

PN WO200220754-A2.

PD 14-MAR-2002.

PF 29-AUG-2001; 2001WO-US027127.

PR 05-SEP-2000; 2000US-0229747P.

PR 05-SEP-2000; 2000US-0229748P.

PR 05-SEP-2000; 2000US-0229749P.

PR 05-SEP-2000; 2000US-0229750P.

PR 05-SEP-2000; 2000US-0229751P.

PR 06-SEP-2000; 2000US-0230583P.

PR 06-SEP-2000; 2000US-0230584P.

PR 06-SEP-2000; 2000US-0230585P.

PR 06-SEP-2000; 2000US-0230586P.

PR 06-SEP-2000; 2000US-0230587P.

PR 06-SEP-2000; 2000US-0230588P.

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PR 06-SEP-2000; 2000US-0230610P.
PR 06-SEP-2000; 2000US-0230865P.
PR 06-SEP-2000; 2000US-0230988P.
PR 07-SEP-2000; 2000US-0230951P.
PR 07-SEP-2000; 2000US-0231163P.
PR 07-SEP-2000; 2000US-0231167P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL;
PI Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR;
PI Miyayama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;
PI Gerstin EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
XX
XX WPI; 2002-383054/41.
DR P-PSDB; ABG60208.
XX
XX An isolated polynucleotide useful in diagnostics and therapeutics.
XX
XX Claim 1; Page 525; 686pp; English.
XX
XX The invention relates to human diagnostic and therapeutic (dithp)
CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal
CC infections, parasitic infections, developmental disorders (e.g. anaemia,
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders
CC (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences
CC ABK1535-ABK71809 represent human dithp polynucleotides of the invention
XX
XX Sequence 643 BP; 173 A; 146 C; 177 G; 147 T; 0 U; 0 Other;
SQ
Query Match 11.3%; Score 144.2; DB 6; Length 643;
Best Local Similarity 85.2%; Pred. No. 9.1e-34;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
Db 95 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 154
QY 190 GTGTATGGCAACATCATCAGGTCAAAACCGAGACAGTGAAGACGACTGTGTCTC 249
Db 155 CCTGACGCGCAACACCTCACCGTCAAAACTGAGAGCAGCGTGAAGACCGCTGTCTTC 214
QY 250 TTGTAACTTGGGAGAGAGTGTGATGAACGACAGCTGATGGCAGAAAACCTGAGTCTCAG 309
Db 215 TTGCACCTTGGGAGAGAGTGTGATGAACCAACAGCTGATGGCAGAAAACCTGAGACGCT 274
QY 310 CTACAACAT 318
Db 275 CTGCACCTT 283
RESULT 7
ADF30639
ID ADF30639 standard; cDNA; 695 BP.
XX
XX ADF30639;
AC
XX 12-FEB-2004 (first entry)
DT
XX Rat angiogenesis modulating protein cDNA #53.
DE
XX ss; gene; rat; angiogenesis; angiogenesis modulating protein;
KW
retinal neovascularisation; choroidal neovascularisation;
chronic inflammation; myocardial ischaemia; stroke;
coronary artery disease; peripheral vascular disease.
Rattus norvegicus.
US2003162706-A1.
XX
XX 28-AUG-2003.
XX
XX 10-DEC-2002; 2002US-00316253.
XX
XX 08-FEB-2002; 2002US-0355295P.
XX
XX 26-JUN-2002; 2002US-0391758P.
XX
XX (PROC ) PROCTER & GAMBLE CO.
XX
XX Peters KG, Thompson LJ, Wang F, Greis KD;
XX
XX WPI; 2003-711557/67.
DR P-PSDB; ADF30640.
XX
XX Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
PT neovascularization or diseases associated with chronic inflammation,
PT myocardial ischemia, stroke, coronary artery disease or peripheral
PT vascular disease.
XX
XX Disclosure; SEQ ID NO 202; 26pp; English.
XX
XX The invention relates to a method of treating an angiogenesis-mediated
CC disorder in a subject. The method is useful for treating angiogenesis-
CC mediated disorder, e.g., retinal or choroidal neovascularisation or
CC diseases associated with chronic inflammation, myocardial ischaemia,
CC stroke, coronary artery disease or peripheral vascular disease. The
CC present sequence is used in the exemplification of the invention.
XX
XX Sequence 695 BP; 194 A; 162 C; 183 G; 156 T; 0 U; 0 Other;
SQ
Query Match 11.3%; Score 144.2; DB 10; Length 695;
Best Local Similarity 85.2%; Pred. No. 9.5e-34;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
Db 136 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 195
QY 190 GTGTATGGCAACATCATCAGGTCAAAACCGAGACAGTGAAGACGACTGTGTCTC 249
Db 196 CCTGACGCGCAACACCTCACCGTCAAAACTGAGAGCAGCGTGAAGACCGCTGTCTTC 255
QY 250 TTGTAACTTGGGAGAGAGTGTGATGAACGACAGCTGATGGCAGAAAACCTGAGTCTCAG 309
Db 256 TTGCACCTTGGGAGAGAGTGTGATGAACCAACAGCTGATGGCAGAAAACCTGAGACGCT 315
QY 310 CTACAACAT 318
Db 316 CTGCACCTT 324
RESULT 8
ADF30635
ID ADF30635 standard; cDNA; 704 BP.
XX
XX ADF30635;
AC
XX 12-FEB-2004 (first entry)
DT
XX Rat angiogenesis modulating protein cDNA #51.
DE
XX ss; gene; rat; angiogenesis; angiogenesis modulating protein;
KW
retinal neovascularisation; choroidal neovascularisation;
chronic inflammation; myocardial ischaemia; stroke;
coronary artery disease; peripheral vascular disease.
```

XX OS Rattus norvegicus.
XX PN US2003162706-A1.
XX PD 28-AUG-2003.
XX PF 10-DEC-2002; 2002US-00316253.
XX PR 08-FEB-2002; 2002US-0355295P.
XX PR 26-JUN-2002; 2002US-0391758P.
XX PA (PROC) PROCTER & GAMBLE CO.
XX PI Peters KG, Thompson LJ, Wang F, Greis KD;
XX WPI; 2003-711557/67.
XX DR P-PSDB; ADF30636.
XX PT Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
PT neovascularization or diseases associated with chronic inflammation,
PT myocardial ischemia, stroke, coronary artery disease or peripheral
PT vascular disease.
XX PS Disclosure; SEQ ID NO 198; 26pp; English.
XX CC The invention relates to a method of treating an angiogenesis-mediated
CC disorder in a subject. The method is useful for treating angiogenesis-
CC mediated disorder, e.g., retinal or choroidal neovascularisation or
CC diseases associated with chronic inflammation, myocardial ischaemia,
CC stroke, coronary artery disease or peripheral vascular disease. The
CC present sequence is used in the exemplification of the invention.
XX SQ Sequence 704 BP; 217 A; 157 C; 178 G; 152 T; 0 U; 0 Other;
Query Match 11.3%; Score 144.2; DB 10; Length 704;
Best Local Similarity 85.2%; Pred. No. 9.5e-34;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGTCCATGGCCAGCCAGACTGTATCATTTAC 189
DB 121 AGGAGTAGGCTGGCTCTTAGGAGATGGTCCATGGCCAAACAGACTGCATCATTTAC 180
QY 190 GTGTGATGCAACAACATCACCGTCAAAACCCGAGACACAGTGAAGACGACTGTGTCTC 249
DB 181 CCTGACGGCAACAACCTCACCGTCAAAACTGAGAGCAGCGTGAAGACGACCGTGTTC 240
QY 250 TTGTAACCTGGAGAGAACTTTGATCAAAACGAGACAGTGAAGACGACTGTGTCTC 309
DB 241 TTGCACTTTGGGAGAGAGTTTGTATGAACCAACAGCTGATGGCAGGAAACTGAGACG 300
QY 310 CTACAAACAT 318
DB 301 CTGCACCTT 309
RESULT 9
ID ADP72791 standard; DNA; 704 BP.
XX AC ADP72791;
XX DT 26-AUG-2004 (first entry)
XX DE Renal toxin progression gene marker #1380.
XX KW ds; toxic effect; gene expression profile; kidney tissue;
XX KW differential gene expression; toxicity progression; toxicity marker;
XX KW drug screening; toxicity assay; kidney pathology; nephritis;
XX KW kidney necrosis; glomerular injury; tubular injury;
XX KW focal segmental glomerulosclerosis.
XX OS Rattus norvegicus.

XX WO2004048598-A2.
XX 10-JUN-2004.
XX 24-NOV-2003; 2003WO-US037556.
XX 22-NOV-2002; 2002US-00301856.
XX (GENE-) GENE LOGIC INC.
XX Mendrick DL, Porter MW, Johnson KR, Castle A, Higgs B;
XX Elashoff M;
XX WPI; 2004-460771/43.
XX Predicting (the progression of) a toxic effect of a compound, for
XX monitoring the progression of renal disease states, comprises preparing a
XX gene expression profile of a kidney tissue or cell sample exposed to the
XX compound.
XX Claim 11; SEQ ID NO 1380; 266pp; English.
XX The invention relates to a method of predicting (the progression of) a
XX toxic effect of a compound by preparing a gene expression profile of a
XX kidney tissue or cell sample exposed to the compound and comparing the
XX gene expression profile to a database, or detecting the level of gene(s)
XX expression in a tissue or cell sample exposed to the compound, where
XX differential gene expression compared to a control indicates a toxic
XX effect (toxicity progression). The method is useful for predicting (the
XX progression of) at least one toxic effect of a compound. The genes are
XX useful as toxicity markers in drug screening and toxicity assays. The
XX methods are useful for predicting the likelihood that a compound or test
XX agent will induce various specific kidney pathologies, such as nephritis,
XX kidney necrosis, glomerular and tubular injury, or focal segmental
XX glomerulosclerosis. The methods are useful for determining the similarity
XX of a toxic response to one or more individual compounds and for
XX predicting or elucidating the potential cellular pathways influenced,
XX induced or modulated by the compound or test agent. The kit is useful for
XX predicting or modelling the toxic response of a test compound, for
XX monitoring the progression of renal disease states, for identifying genes
XX that show promise as new drug targets and for screening known and newly
XX designed drugs. This sequence corresponds to a gene marker used in the
XX method of the invention. (Note: The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences).
XX SQ Sequence 704 BP; 217 A; 157 C; 178 G; 152 T; 0 U; 0 Other;
Query Match 11.3%; Score 144.2; DB 12; Length 704;
Best Local Similarity 85.2%; Pred. No. 9.5e-34;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGTCCATGGCCAGCCAGACTGTATCATTTAC 189
DB 121 AGGAGTAGGCTGGCTCTTAGGAAGATGGTCCATGGCCAAACAGACTGCATCATTTAC 180
QY 190 GTGTGATGCAACAACATCACCGTCAAAACCCGAGACACAGTGAAGACGACTGTGTCTC 249
DB 181 CCTGACGGCAACAACCTCACCGTCAAAACTGAGAGACCGTGAAGACGACCGTGTTC 240
QY 250 TTGTAACCTGGGAGAGAACTTTGATGAACCGAGCTGATGGCAGAAAACTGAGGTCTAG 309
DB 241 TTGCACCTTTGGGAGAGAGTTTGTATGAACCAACAGCTGATGGCAGGAAACTGAGACG 300
QY 310 CTACAAACAT 318
DB 301 CTGCACCTT 309
RESULT 10
ID ADB53766 standard; DNA; 664 BP.

XX ADB53766;
AC
XX
XX
DT 04-DEC-2003 (first entry)
XX
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4308.
XX
XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; db.
XX
OS Rattus norvegicus.
XX
XX
XX WO2003065993-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-US003482.
XX
XX 04-FEB-2002; 2002US-0353171P.
PR 13-MAR-2002; 2002US-0363534P.
PR 08-APR-2002; 2002US-0370248P.
PR 10-APR-2002; 2002US-0371134P.
PR 10-APR-2002; 2002US-0371135P.
PR 10-APR-2002; 2002US-0371150P.
PR 11-APR-2002; 2002US-0371413P.
PR 19-APR-2002; 2002US-0373601P.
PR 19-APR-2002; 2002US-0373602P.
PR 22-APR-2002; 2002US-0374139P.
PR 08-MAY-2002; 2002US-0378370P.
PR 09-MAY-2002; 2002US-0378652P.
PR 09-MAY-2002; 2002US-0378653P.
PR 09-MAY-2002; 2002US-0378665P.
PR 09-JUL-2002; 2002US-0394230P.
PR 09-JUL-2002; 2002US-0394253P.
PR 04-SEP-2002; 2002US-0407688P.
PR 28-JAN-2003; 2003US-0442900P.
XX
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
PI Elashoff M;
XX
XX WPI; 2003-731472/69.
XX
XX Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
XX Claim 44; SEQ ID NO 4308; 874pp; English.
XX
XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
XX Sequence 664 BP; 180 A; 152 C; 178 G; 154 T; 0 U; 0 Other;
SQ
Query Match 11.1%; Score 142.6; DB 10; Length 664;
Best Local Similarity 84.7%; Pred. No. 2.9e-33;
Matches 160; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 189
119 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 178
130 GTGTGATGGCAACACATCAGGTCACAAACCGAGAGCAGCAGTGAAGACGACTGTCTTC 249
179 CCTGACACACACACACCTCACCGTCAAACTGAGAGCAGCAGTGAAGACGACCGTGTTC 238
250 TTGTAACCTGGAGAGAGAGTTTGTATGAACACACAGCTGATGSCAGAAAACCTGAGGTG 309
239 TTGCACCTTGGAGAGAGAGTTTGTATGAACACACAGCTGATGSCAGAAAACCTGAGACGGT 298
310 CTACAACAT 318
299 CTGCACCTT 307
RESULT 11
ADP30637
ID ADF30637 standard; cDNA; 664 BP.
XX
AC ADF30637;
XX
DT 12-FEB-2004 (first entry)
XX
DE Rat angiogenesis modulating protein cDNA #52.
XX
KW ss; gene; rat; angiogenesis; angiogenesis modulating protein;
KW retinal neovascularisation; choroidal neovascularisation;
KW chronic inflammation; myocardial ischaemia; stroke;
KW coronary artery disease; peripheral vascular disease.
XX
OS Rattus norvegicus.
XX
XX US2003162706-A1.
XX
XX 28-AUG-2003.
XX
XX 10-DEC-2002; 2002US-00316253.
XX
XX 08-FEB-2002; 2002US-0355295P.
PR 26-JUN-2002; 2002US-0391758P.
XX
XX (PROC) PROCTER & GAMBLE CO.
XX
XX Peters KG, Thompson LJ, Wang F, Greis KD;
XX
XX WPI; 2003-711557/67.
DR P-PSDB; ADF30638.
XX
XX Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
PT neovascularization or diseases associated with chronic inflammation,
PT myocardial ischemia, stroke, coronary artery disease or peripheral
PT vascular disease.
XX
XX Disclosure; SEQ ID NO 200; 26pp; English.
XX
XX The invention relates to a method of treating an angiogenesis-mediated
CC disorder in a subject. The method is useful for treating angiogenesis-
CC mediated disorder, e.g., retinal or choroidal neovascularisation or
CC diseases associated with chronic inflammation, myocardial ischaemia,
CC stroke, coronary artery disease or peripheral vascular disease. The
CC present sequence is used in the exemplification of the invention.
XX
XX Sequence 664 BP; 180 A; 152 C; 178 G; 154 T; 0 U; 0 Other;
SQ
Query Match 11.1%; Score 142.6; DB 10; Length 664;
Best Local Similarity 84.7%; Pred. No. 2.9e-33;
Matches 160; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 189
119 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 178

QY 190 GTGTGATGGCAACATCATCGGTCAAAACCCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 179 CTTGACAAACAACTCACCCTCAAACTGAGAGCAGTGAAGACGACCGTGTCTC 238
QY 250 TTGTACCTGGGAGAGAACTTTGATCAAAACGACAGCTGTGAGAGAACTGAGTCA 309
DB 239 TTGCACCTTGGGAGAGAACTTTGATCAAAACGACAGCTGTGAGAGAACTGAGTCA 298
QY 310 CTACACAT 318
DB 299 CTGCACCTT 307

RESULT 12
ID ABL92950/c
XX ABL92950 standard; cDNA; 335 BP.
AC ABL92950;
XX
DT 10-JUN-2002 (first entry)
XX
DE Rat metastatic tumour cell related cDNA SEQ ID NO 4.
XX
KW Metastatic: tumour; breast cancer; pancreatic cancer; cytostatic; ss.
XX
OS Rattus sp.
XX
PN WO200208456-A2.
XX
PD 31-JAN-2002.
XX
PF 24-JUL-2001; 2001WO-EP008517.
XX
PR 25-JUL-2000; 2000DE-01036126.
XX
PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
XX
PI Von Stein O, Nestl A, Hofmann M, Sleeman J, Herrlich P;
XX
DR WPI; 2002-172012/22.
XX
XX Identifying metastatic tumor cells and screening for antitumor agents,
PT comprises hybridization to specific cDNA sequences.
XX
PS Disclosure; Page 27-28; 140pp; German.
XX
CC The invention relates to identifying metastatic tumour cells comprising
CC testing them for hybridisation to at least one cDNA sequence (ABL92947-
CC ABL93235) or the derived complete gene, functional fragments, homologues
CC or alleles. The cDNA sequences are markers for metastatic potential in
CC breast and pancreatic tumours, useful for diagnosis, particularly for
CC staging cancers and selection of therapy and used for identifying
CC potential agents for treatment of cancer, e.g. antibodies against
CC proteins encoded by the cDNA sequences or antisense sequences. The cDNA
CC sequences are also used to clone the complete gene, allowing its
CC functional analysis, including study of metastasis-specific regulatory
CC sequences for clarification of molecular regulatory mechanisms of
CC metastasis
XX
SQ Sequence 335 BP; 59 A; 101 C; 68 G; 104 T; 0 U; 3 Other;

Query Match 10.1%; Score 129.8; DB 6; Length 335;
Best Local Similarity 82.2%; Pred. No. 1.9e-29;
Matches 157; Conservative 3; Mismatches 30; Indels 1; Gaps 1;

QY 130 AGGAGTAGGCTGGCTCTTAGGAGATGGCTGCC-ATGCGCCAGCCAGACTGTATCATTA 188
DB 305 AGGAGTAGGCTGGCTCTTAGGAGATGGCTGMAATGGCCAAACCCAGACTGCATCATTA 246
QY 189 CGTGTGATGGCAACATCATCGGTCAAAACCCGAGAGCAGTGAAGACGACTGTCTT 248
DB 245 CCTAGACGGCAACCACTCACCCTGTAAGAGCAGCGGTGAAGAGCCGCTGTTT 186

QY 249 CTTGTAACTGGGAGAGAACTTTGATGAACACGACCTGATGCGAGAAACCTGAGTCA 308
DB 185 CTTGCACCTGGGAGAGAACTTTGATGAACACGACCTGATGCGAGAAACCTGAGACGG 126
QY 309 GCTACACATA 319
DB 125 TCTGCACCTTA 115

RESULT 13
ID ADN07741/c
XX ADN07741 standard; cDNA; 335 BP.
AC ADN07741;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human mammary carcinoma MLSSH cDNA library sequence #4.
XX
KW Human; ss; mammary carcinoma; metastasis; cancer; tumour; Metastachip;
KW suppressive subtractive hybridisation; MLSSH; breast cancer;
KW metastatic potential.
XX
OS Homo sapiens.
XX
PN DE10229391-A1.
XX
PD 29-JAN-2004.
XX
PF 29-JUN-2002; 2002DE-01029391.
XX
PR 29-JUN-2002; 2002DE-01029391.
XX
PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
XX
PI Sleemann J, Herrlich P;
XX
DR WPI; 2004-134410/14.
XX
PT Biochip, useful for identifying metastatizing tumors and assessing
PT metastatic potential, carries cDNA copies of genes with metastasis-
PT specific expression and of control genes.
XX
PS Disclosure; Fig A; 237pp; German.
XX
CC The invention relates to a biochip (termed a Metastachip) comprising,
CC arranged on a carrier, cDNA copies of genes, or their fragments, for
CC which expression is altered in metastasis and as controls, cDNA copies of
CC genes, or their fragments, for which expression is not altered in
CC metastasis. Also included is a method for identifying metastasising
CC tumours by screening genetic markers of the tumour with the new biochip.
CC The genes are derived from malignant cells, preferably from a tumour-
CC specific library, especially of breast/mammary carcinoma. The
CC specification lists sequences of cDNA copies present in a breast
CC carcinoma library and a pancreas-specific library, containing about 160
CC and 120 sequences, reproduced. They are produced by suppressive
CC subtractive hybridisation (MLSSH pr PLSSH sequences). The biochip is used
CC to identify metastatic tumours and to determine the degree of metastatic
CC potential, particularly of breast carcinoma. The determination, also the
CC characterisation of the progression of metastasis, may be qualitative or
CC quantitative. The biochip is simple to prepare, has a low error rate and
CC suffers few interferences. The presence of control sequences ensures that
CC determination of expression is tumour- and tissue-specific, even patient-
CC specific, and the effects of measurement errors and of artifacts of data
CC processing are minimised. The present sequence is a Human mammary
CC carcinoma MLSSH cDNA library sequence for the biochip.
XX
SQ Sequence 335 BP; 59 A; 101 C; 68 G; 104 T; 0 U; 3 Other;

Query Match 10.1%; Score 129.8; DB 12; Length 335;
Best Local Similarity 82.2%; Pred. No. 1.9e-29;
Matches 157; Conservative 3; Mismatches 30; Indels 1; Gaps 1;

QY 130 AGGACTAGACTGGCTCTTAGAAGATGGCTGCC-ATGCCAAGCCAGACTGTATCATTA 188
|||||
Db 305 AGGAGTAGGGCTGGCTCTTAGGGAGATGGGTGCMATGGCCAAACCCAGACTGCATCATTA 246
|||||
QY 189 CGTGTGATGGCAACAAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCT 248
|||||
Db 245 CCCTAGACGGCNAACCTCACCGTMAAACTGAGAGCACGGTGAAGAMGACCGTGT 186
|||||
QY 249 CTTGTAACCTGGAGAGAAAGTTTGATGAAACGACAGCTGATGGCAGAAAAAATGAGGTCA 308
|||||
Db 185 CTTGCACCTTGGAGAGAAAGTTTGATGAAACCCACAGCTGATGGCAGGAAAAATGAGACGG 126
|||||
QY 309 GCTACAAATA 319
|||||
Db 125 TCTGCACCTTA 115
|||||
RESULT 14
AAQ66842
ID AAQ66842 standard; DNA; 408 BP.
XX
AC AAQ66842;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1994 (first entry)
XX
DE Melanogenic inhibitor.
XX
KW Melanogenic inhibitor; MI; melanogenesis; melanin; pigment;
KW depigmentation; melanoma; ss.
XX
OS Homo sapiens.
XX
FH Key
FT 1. .408
FT CDS /*tag= a
XX
XX WO9412534-A2.
PD
PD 09-JUN-1994. 93WO-US011139.
PF
PF 16-NOV-1993;
XX
XX 24-NOV-1992; 92US-00980513.
PR 01-SEP-1993; 93US-00115172.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Nordlund JJ, Farooqui JZ;
XX
XX WPI; 1994-200198/24.
DR P-PSDB; AAR55866.
XX
XX Prodn. of a protein for inhibiting melanogenesis - useful for treating
PT hyper-pigmentary diseases, destroying melanoma cells and for lightening
PT unwanted body hair.
XX
PS Disclosure; Page 3-4; 40pp; English.
XX
XX PCR primers given in AAQ66843-44 were used to amplify RNA from human skin
CC previously grafted onto nude mice, thereby providing DNA (AAQ66842)
CC encoding melanogenic inhibitor protein (AAR55866). (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 408 BP; 142 A; 67 C; 111 G; 88 T; 0 U; 0 Other;

Query Match 9.8%; Score 125; DB 2; Length 408;
Best Local Similarity 78.8%; Pred. No. 6.8e-28;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 130 AGGAGTAGACTGGCTCTTAGAAGATGGCTGCCAAGCCAGACTGTATCATTA 189
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Db 78 AGGAGTGGAAATAGCTTTTCCGAAAAAATGGCGCAATGGCCCAAGCCAGATTGTATCATCAC 137
QY 190 GTGTGATGGCAACACATCACGGTCAAAACCGAGAGCACAGTGAAGACGAGCTGTCTTCTC 249
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Db 138 TTGTGATGGTAAAAACCTCACCATAAAAAACTGAGAGCACTTTTGAANAACACACAGCTTTTC 197
|||||
QY 250 TTGTAACCTGGGAGAGAAAGTTTGATGAAACACACAGCTGATGGCAGAAAAAATCTGAGGTGAG 309
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Db 198 TTGTACCTGGGAGAGAAAGTTTGAAGAAACCCACAGCTGATGGCAGAAAAAATCTCAGACTGT 257
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QY 310 CTACAACAT 318
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Db 258 CTGCAACTT 266
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RESULT 15
ABK53980
ID ABK53980 standard; cDNA; 461 BP.
XX
AC ABK53980;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human head and neck tumour cDNA, SEQ ID No 175.
XX
KW Human; head and neck cancer; tumour; cytostatic; immunogenic; vaccine;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO200212329-A2.
XX
PD 14-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024226.
XX
PR 03-AUG-2000; 2000US-0223281P.
PR 16-NOV-2000; 2000US-0249933P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Wang T, Fan L;
PI
XX WPI; 2002-257467/30.
DR
XX Novel polynucleotide encoding head and neck tumor polypeptides, useful in
PT pharmaceutical compositions, e.g. vaccines, for treating head and neck
PT cancers.
XX
PS Claim 1; Page 167; 200pp; English.

XX The invention relates to an isolated polynucleotide (I) comprising
CC sequences selected from 273 sequences fully defined in the specification.
CC (I), including its encoded polypeptide (II), an antibody binding to (II),
CC a fusion protein comprising (II) and a T-cell population stimulated by
CC (I) or (II) are useful for stimulating an immune response in a patient
CC and treating head and neck cancer in a patient. An oligonucleotide (III)
CC that hybridises to (I) is useful for determining the presence of cancer
CC in a patient, by obtaining a biological sample from the patient,
CC contacting the sample with (III), detecting in the sample an amount of a
CC polynucleotide that hybridises to the oligonucleotide, and comparing the
CC amount of polynucleotide that hybridises to the oligonucleotides to a
CC predetermined cut-off value. (I) and (II) are useful in pharmaceutical
CC compositions, e.g. vaccines, and other compositions for the diagnosis and
CC treatment of head and neck cancer. ABK53806-ABK54078 represent human head
CC and neck cancer cDNA sequences of the invention
XX
SQ Sequence 461 BP; 153 A; 91 C; 119 G; 96 T; 0 U; 2 Other;

Query Match 9.8%; Score 125; DB 6; Length 461;
Best Local Similarity 78.8%; Pred. No. 7.3e-28;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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QY 1261 CTATGAGAGGTGCAATGA 1279
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DEFINITION AJ223066
VERSION AJ223066.1 GI:3183984
KEYWORDS E-FABP; epidermal protein; Fabpe gene; fatty acid binding protein.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Bleck, B., Hohoff, C., Binas, B., Rustow, B., Dixkens, C., Hameister, H., Borchers, T. and Spener, F.
TITLE Cloning and chromosomal localisation of the murine epidermal-type fatty acid binding protein gene (Fabpe)
JOURNAL Gene 215 (1), 123-130 (1998)
MEDLINE 98332726
PubMed 9666100
REFERENCE 2
AUTHORS Spener, F.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1997) Spener F., Department of Biochemistry, University of Muenster, Wilhelm-Klemm-Str. 2, D-48149, GERMANY
REMARK Revised by [3]
AUTHORS 3 (bases 1 to 6593)
Spener, F. and Bleck, B.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1998) Spener F., Department of Biochemistry, University of Muenster, Wilhelm-Klemm-Str. 2, D-48149, GERMANY
COMMENT On Jun 4, 1998 this sequence version replaced gi:2760452.
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 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
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 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
 Weinstock, G. and Gibbs, R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 234778)
 Worley, K.C.
 Direct Submission
 Submitted (09-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 234778)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 10, 2003 this sequence version replaced gi:23321796.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GILZ
 Center clone name: CH230-189N20
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 214384 bases at least Q40
 Consensus quality: 217402 bases at least Q30
 Consensus quality: 219588 bases at least Q20
 Estimated insert size: 224004; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 consists of 9 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 *
 * 136852: contig of 136852 bp in length
 * 136853 136952: gap of unknown length
 * 136953 147544: contig of 10592 bp in length
 * 147545 147545: gap of unknown length
 * 147545 177489: contig of 29844 bp in length
 * 177489 177588: gap of unknown length
 * 177589 227081: contig of 49493 bp in length
 * 227082 227181: gap of unknown length
 * 227182 228199: contig of 1018 bp in length
 * 228200 228300: gap of unknown length
 * 228301 229308: contig of 1009 bp in length
 * 229309 229408: gap of unknown length
 * 229409 230448: contig of 1040 bp in length
 * 230449 230548: gap of unknown length
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 Db 171568 TACTGTGCAATGATTAACCGACCTTATGCTTTCTCCGCTCTGAGGAGTAGGCTGGC 171627
 QY 145 TCTTAGGAGATGGTGGCCATGCGCAAGCAGACTGTATCATTCGTGTGATGGCAACAA 204
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 QY 564 GAGTGTGTGGGTCTCTGGGGTTCCTTCACTTTTGAAGATGATGAACCTACCTACCTGTA 623

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Db 172208 GAAGTGTT--TATCATGCTGGCATTTCTGCTTGCAGCCACTTGTTCACA----- 172253
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LOCUS Homo sapiens chromosome 8 clone CTB-402C7 map 8q21-q23, complete
DEFINITION sequence.
ACCESSION AF181449
VERSION AF181449.3 GI:22091331
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 42874)
AUTHORS Blechschmidt,K., Schattevoy,R., Baumgart,C. and Rosenthal,A.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 42874)
AUTHORS Blechschmidt,K., Schilhabel,M., Schattevoy,R., Baumgart,C.,
Menzel,J., Weber,J., Korenberg,J.R. and Rosenthal,A.
Direct Submission
TITLE Submitted (23-AUG-1999) Genome Analysis, Institute of Molecular
JOURNAL Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE 3 (bases 1 to 42874)
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AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Schilhabel,M.B. and Platzter,M.
Direct Submission
Submitted (07-JUN-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
4 (bases 1 to 42874)
Lagemann,D. and Platzter,M.
Direct Submission
Submitted (02-AUG-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
On Aug 2, 2002 this sequence version replaced gi:14327843.
----- Genome Center
Center: Institute of Molecular Biotechnology
Center code: IMB
Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
----- Project Information
Center project name: H193
Center clone name: CTB-402C7
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 42771 bases at least Q40
Consensus quality: 42810 bases at least Q30
Consensus quality: 42843 bases at least Q20
Quality coverage: 31.66x

This sequence was finished as follows unless otherwise noted: all
regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest.

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.

FEATURES
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ORGANISM Homo sapiens
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AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Homo sapiens, clone RP11-28G10
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 174316)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
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Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 6, 2001 this sequence version replaced gi:13184149.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

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----- Project Information

Center project name: L4751

Center clone name: 28_G.10

----- Summary Statistics

Sequencing vector: M13; M77815; 3% of reads

Chemistry: Dye-terminator Big Dye; 97% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 172808 bases at least Q40

Consensus quality: 173594 bases at least Q30

Consensus quality: 173848 bases at least Q20

Insert size: 170000; agarose-fp

Insert size: 174016; sum-of-contigs

Quality coverage: 8.3 in Q20 bases; agarose-fp

Quality coverage: 8.1 in Q20 bases.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.

* as soon as it is available and the accession number will

* be preserved.

* * * * *

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* 2693 2792: gap of 100 bp

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RESULT 7

AC009902/c

LOCUS

DEFINITION

AC009902

ACCESSION

VERSION

217249 bp DNA linear PRI 18-OCT-2002

Homo sapiens chromosome 8, clone RP11-363E6, complete sequence.

AC009902

AC009902.13 GI:24111046

KEYWORDS	HTG.	TITLE	Direct Submission
SOURCE	Homo sapiens (human)	JOURNAL	Submitted (18-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
ORGANISM	Homo sapiens	COMMENT	On Oct 18, 2002 this sequence version replaced gi:18250063. All repeats were identified using RepeatMasker:
REFERENCE	1 (bases 1 to 217249)		Smit, A.F.A. & Green, P. (1996-1997)
AUTHORS	Birren, B., Nusbaum, C. and Lander, E.		http://ftp.genome.washington.edu/RM/RepeatMasker.html
TITLE	Homo sapiens chromosome 8, clone RP11-363E6		----- Genome Center
REFERENCE	2 (bases 1 to 217249)		Center: Whitehead Institute/ MIT Center for Genome Research
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Depayre, E., Devon, K., Dewar, K., Doneelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Jones, C., Kann, L., Karatas, A., Lehocsky, J., Liu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J. and Zody, M.		----- Center code: WIBR Web site: http://www-seq.wi.mit.edu Contact: sequence.submissions@genome.wi.mit.edu ----- Project information Center project name: L2420 Center clone name: 363_E_6 -----
TITLE	Direct Submission	FEATURES	Location/Qualifiers
JOURNAL	Submitted (05-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Source	1. 217249
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QY	246 TCTCTTGTAACTGGGAGAGAGTTTGATGAACGACAGCTGATGGCAGAAAACTGAGG 305
Db	71257 TTTCTTGTACCTGGGAGAGAGTTTGAAGAAACCAACAGCTGATGGCAGAAAACTCAGG 71198
QY	306 TCAGCTACAACTACTGTGAAGCGACAGAGCTTCTAGATTTCACAGATTAAATTGCATTA 365
Db	71197 TCAGTCGTGACATGTTATGAATACAGAGCTTCTAGATGATAGCTGTAT--CAAT 71141
QY	366 ACAATCTCTGTACTTACTGCCAAGGGCTGACTGAAAAAACTACTTTATCGAGTTGACTTT 425

Db	71140 AACATTTTACTGTTTTATAGGCAAGAACTTAATGAAAAAGTTATTTTAT-GAATTGAATTT 71082
QY	426 TGATAAATTTAGTAAAGTCCAGGACTAAGAAATCAAGACACTCTTATGAGTTTCTAGATC 485
Db	71081 TGTCAAATTTAGCAAAAGTATCAACTTCATCATGAATTTGGCATCTTTTATTAGCTACTAG 71022
QY	486 GAAAAGCACATAGTTGTATGTGAACAAAAACAGTATGATGGGTGGAGT----TCAGAG 541
Db	71021 GTTGAANAACCAAAACTATTGTGAATAAAATCAATATGGTTTAATGAAGTAGACTCAGAA 70962
QY	542 AGGGAAGCGCAAGACTTGTGGAGT-----GGTGTGGTCTCTGGGGTCTCTTCACTT 595
Db	70961 AGGAGAGGTGAACAATAATGTTGATTAAGGAGGTTATGAGTCATGGAACCTCTTGAATG 70902
QY	596 TGGAGATGATGAACCTAACTACCTCCCTGTATTTTGCAGACGGTCTGCACCTTCCAAGACGG 655
Db	70901 TACTTTGGAAGATTAAACGTTTACTTTTGTTTTTCAGACTGTCTGCAACTTTTACAGATGG 70842
QY	656 TGCCCTGTGTCAGCACCAAGCAATGGGCGGGAAGAGAGACGATAAACAAGAAAACTGAA 715
Db	70841 TGCATTGGTTCAGCATCAGGAGTGGATGGGAAGGAAAGCAACAATAACAAGAAAAATTGAA 70782
QY	716 GGAATGGGAAGATGATCGTGTGAGCATCAAGACACTGGCACCATCTCTGGGATTTGGCCCTG 775
Db	70781 AGATGGGAAATTTAGTGGTGGTAAAGTGTCAAACTGCTGTCTCAGTCAGCTTCTTGTGTG 70722
QY	776 CAGCCACAGTTGTCTATAACCACTTCGGGTCTTGTGTTCTTTTAAACAAGAGAAGAACTTA 835
Db	70721 CATTCTATGTTTACATAACTGTTCTATATCATTTGATCAIT-----AACAGACTCAGTTTG 70666
QY	836 GGAGGACAACTACTGAAAAATAACAAGTTAGAAACGAGAGTCTCTCATTTGTAGGCGACCT 895
Db	70665 GAAAGAAAAAAGCAAAATAACAAGTTAAATACTAGAACACTAAATTTATTAAAGAAAGTCCT 70606
QY	896 TGTGGGACGGAGAAAGTGAATGG-----ATCCAGAGATGGCTGCAGCAGACGCTG---- 947
Db	70605 AGTGAGAGATAGAGAAAGTGCATGACATAGGAGAGGATTTGGCTGGAGTTGGGGGGAGTTC 70546
QY	948 -----AGAGCTGGCAGGCCAGCCAGCAGCCCTCTCTCTGCT 982
Db	70545 TTGCTTTTGTGCCACGTCACAGTGAATCTTGGCAAGCCACCAACTGCACACATTTTC 70486
QY	983 ACAITGATTTAAGTAAGGATATTTGCCAAAAACAATGAATAATTTAGAGATCATATCCA 1042
Db	70485 TATACTCTTTAAATAAAGGAATATTTGCCATAACCAAAAGATAAAGATATATTCAACACA 70426
QY	1043 GTGCTTTAGTCTGAGGCGAGCAATATATACATATAAACAACACAGCAGCTCTAGGCTTT- 1101
Db	70425 TTAGTTTTTCTGTAAAACATGTCATATTATAAGCAAAACAACAGCTTCTGCTCTCTCAAA 70366
QY	1102 CTTGAGTTTGAATCCTGAGATGTTGTTTTCTGTTAGTTGGTTTGTATCAAGCGTTTATAGGA 1161
Db	70365 CCGTGAAATCTGAAAGAAATTTTCTCCATCTATGAGTAGATTAAGTATTTCGTGGGA 70306
QY	1162 TTCTGCC-----ACAAACATGCTCTGAAATGTACAGTTGGCTGTGAGCTC 1208
Db	70305 CTTTGATCTTAATGTTTTTAATACCACACTGCTCTGGAATCTAAGGCTAAACCTAACTCTT 70246
QY	1209 T-----ATCTTTCTCTCTAGGAGTGTGTATGAACATGCCACTGCACCTGCGGCTCTA 1263
Db	70245 TTAATATCTTCTCTCTAGGAGTGTGTATGAACATGTCACCTGTACTCGGATCTA 70186
QY	1264 TCAGAGGTTGCAATGA 1279
Db	70185 TGAANAAGTAGAATAA 70170

RESULT 8	
LOCUS	CQ777551
DEFINITION	Sequence 1237 from Patent EP1394274.
ACCESSION	CQ777551
VERSION	CQ777551.1 GI:45380535
	933 bp DNA linear PAT 11-MAR-2004

KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE	1
AUTHORS	Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Negai, H. and Izuwara, K.
TITLE	Methods of testing for bronchial asthma or chronic obstructive pulmonary disease
JOURNAL	Patent: EP 1394274-A 1237 03-MAR-2004; Genox Research, Inc. (JP)
FEATURES	Location/Qualifiers
source	1..933 /organism="Mus musculus" /mol_type="unassigned DNA" /db_xref="taxon:10090"
ORIGIN	
Query Match	13.8%; Score 176.6; DB 6; Length 933;
Best Local Similarity	95.3%; Pred. No. 2.7e-41;
Matches 182; Conservative	0; Mismatches 9; Indels 0; Gaps 0;
QY	130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db	112 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 171
QY	190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGATGAAGACGACTGTGTTCTC 249
Db	172 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGATGAAGACGACTGTGTTCTC 231
QY	250 TTGTAACCTGGGAGAGAAGTTTGATGAACAGCAGCTGATGCAGAAAACTGAGTCCAG 309
Db	232 TTGTAACCTGGGAGAGAAGTTTGATGAACAGCAGCTGATGCAGAAAACTGAGACGGT 291
QY	310 CTACACATAC 320
Db	292 CTGCACCTTCC 302
RESULT 9	
MMALL	
LOCUS	M.musculus mall mRNA for keratinocyte lipid-binding protein.
DEFINITION	X70100
ACCESSION	X70100.1
VERSION	GI:287985
KEYWORDS	keratinocyte lipid-binding protein.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	1
AUTHORS	Krieg, P., Feil, S., Furstenberger, G. and Bowden, G.T.
TITLE	Tumor-specific overexpression of a novel keratinocyte lipid-binding protein. Identification and characterization of a cloned sequence activated during multistage carcinogenesis in mouse skin
JOURNAL	J. Biol. Chem. 268 (23), 17362-17369 (1993)
MEDLINE	93352523
PUBMED	8349619
REFERENCE	2 (bases 1 to 933)
AUTHORS	Krieg, P.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAR-1993) P. Krieg, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, 6904 Heidelberg, FRG
FEATURES	Location/Qualifiers
source	1..933 /organism="Mus musculus" /mol_type="mRNA" /strain="NMRI" /db_xref="taxon:10090" /clone="p1106, ML2" /cell_type="papilloma, squamous cell carcinoma" /tissue_type="skin" /clone_lib="papilloma cDNA squamous cell carcinoma cDNA"
dev_stage="adult"	1..933
/gene="mall"	1..933
/note="large transcript"	1..655
/note="small transcript"	35..442
/codon_start=1	
/product="keratinocyte lipid-binding protein"	
/protein_id="CAA49703.1"	
/db_xref="GI:287986"	
/db_xref="GOA:Q05816"	
/translation="NASLKDLGKWLMEHGFEEYMKELGVGLARKNAAKPDCCI	
ITCDGNNTVKTSTVTKTVFSCNIGKPFDETDAGRTKTETVCTFDGALVHQHQWDG	
KESTITRKLDGKGMIVCEVMNATCTRVKQV"	
QY	130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db	112 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 171
QY	190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGATGAAGACGACTGTGTTCTC 249
Db	172 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGATGAAGACGACTGTGTTCTC 231
QY	250 TTGTAACCTGGGAGAGAAGTTTGATGAACAGCAGCTGATGCAGAAAACTGAGTCCAG 309
Db	232 TTGTAACCTGGGAGAGAAGTTTGATGAACAGCAGCTGATGCAGAAAACTGAGACGGT 291
QY	310 CTACACATAC 320
Db	292 CTGCACCTTCC 302
RESULT 10	
BC002008	
LOCUS	Mus musculus fatty acid binding protein 5, epidermal, mRNA (cDNA
DEFINITION	Clone MGC:5786 IMAGE:3490535), complete cds.
ACCESSION	BC002008
VERSION	BC002008.1
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	1 (bases 1 to 713)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, I., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richardson, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 JOURNAL

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
 2 (bases 1 to 713)
 Strausberg, R.
 Direct Submission
 Submitted (31-JAN-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Lothar Hengnighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clon distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 8 Row: m Column: 7
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6754449.
 Location/Qualifiers
 1. .713
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="mix FVB/N, C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MGC:5786 IMAGE:3490535"
 /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
 old, gross tissue."
 /clone_lib="NCI CGAP_Mam5"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"
 1. .713
 /gene="Fabp5"
 /note="synonym: mall"
 /db_xref="LocusID:16592"
 /db_xref="MGI:101790"
 36. _443
 /gene="Fabp5"
 /codon_start=1
 /product="fatty acid binding protein 5, epidermal"
 /protein_id="AAH02008.1"
 /db_xref="GI:12805103"
 /db_xref="LocusID:16592"
 /db_xref="MGI:101790"
 /translation="MASLKDLGKRLMESHFESYMKELGVGLRLRYMAWAKPDCI
 ITCDDNNITVTESTVTFTVFCNLGKPFDETTADGRKTETVCTFDGALVQHQQWDG
 KESTITRLKDKGMIVCEVMNATCTRYEVQV"

ORIGIN
 Query Match 13.7%; Score 175; DB 10; Length 713;
 Best Local Similarity 94.8%; Pred. No. 7.8e-41;
 Matches 181; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 172
 Db 113 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 172
 QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGACACAGTGAAGACCACTGTGTTCTC 249
 Db 173 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGACACAGTGAAGACCACTGTGTTCTC 232
 QY 250 TTGTAACCTGGGAGAGAGTTTGTATGAAACGACAGCTGATGGCAGAAAAAAGCTGAGTCTAG 309

Db 233 TTGTAACCTGGGAGAGAGTTTGTATGAAACGACAGCTGATGGCAGAAAAAAGCTGAGACGCT 292
 QY 310 CTACAAACATAC 320
 Db 293 CTGCACCTTCC 303

RESULT 11
 AC125321 196150 bp DNA linear ROD 25-NOV-2003
 LOCUS Mus musculus BAC clone RP23-371B13 from chromosome 9, complete
 DEFINITION sequence.
 ACCESSION AC125321
 VERSION AC125321.4 GI:37951467
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 196150)
 Berghoff, A., Haglund, K., Kozlowicz, A., Bielicki, L. and Meyer, R.
 The sequence of Mus musculus BAC clone RP23-371B13
 Unpublished (2001)
 REFERENCE 2 (bases 1 to 196150)
 AUTHORS Wilson, R.
 TITLE Sequencing of Mus musculus
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 196150)
 AUTHORS McPherson, J.D. and Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (22-JUN-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 196150)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (06-AUG-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 196150)
 AUTHORS Wilson, R.K.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 6 (bases 1 to 196150)
 AUTHORS Wilson, R.
 TITLE Direct Submission
 JOURNAL Submitted (25-NOV-2003) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Oct 24, 2003 this sequence version replaced gi:33457280.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu>
 Contact: submissions@watson.wustl.edu
 ----- Summary Statistics

 Center project name: M_BA0371B13

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:
 Mapping information for this clone was provided by Dr. Wes Warren,

QY 190 GTGTGTCGCAACAATCAGCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 249
 |||||
 Db 182112 GTGTGTCGCAACAATCAGCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 182171
 |||||

QY 250 TTGTAACTGGGAGAGAGTTTGATGAACGACGACGCTGATGCGAGAAAACCTGAG 304
 |||||
 Db 182172 TTGTAACTGGGAGAGAGTTTGATGAACGACGACGCTGATGCGAGAAAACCTGAG 182226
 |||||

RESULT 12
 AC124432/c
 LOCUS AC124432 160728 bp DNA linear ROD 27-NOV-2003
 DEFINITION Mus musculus BAC clone RP24-243L15 from chromosome 18, complete
 sequence.
 AC124432
 VERSION AC124432.5 GI:31194018
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 160728)
 AUTHORS Swearingen-Shahid, S. and Meyer, R.
 JOURNAL The sequence of Mus musculus BAC clone RP24-243L15
 Unpublished (2001)
 REFERENCE 2 (bases 1 to 160728)
 AUTHORS Wilson, R.
 TITLE Sequencing of Mus musculus
 JOURNAL Unpublished (2001)
 REFERENCE 3 (bases 1 to 160728)
 AUTHORS McPherson, J.D. and Waterston, R.H.
 JOURNAL Direct Submission
 Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 4 (bases 1 to 160728)
 AUTHORS McPherson, J.D. and Waterston, R.H.
 JOURNAL Direct Submission
 Submitted (02-APR-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 5 (bases 1 to 160728)
 AUTHORS Wilson, R.K.
 JOURNAL Direct Submission
 Submitted (30-MAY-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE 6 (bases 1 to 160728)
 AUTHORS Wilson, R.
 JOURNAL Direct Submission
 Submitted (27-NOV-2003) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On May 30, 2003 this sequence version replaced gi:29469630.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu
 Contact: submissions@watson.wustl.edu
 ----- Summary Statistics

 Center project name: M_BB0243L15

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,
 Department of Genetics, Washington University, St. Louis MO. For
 additional information about the map position of this sequence, see
 http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and
 coworkers (http://www.chori.org) from male C57BL/6J mouse spleen
 and/or brain genomic DNA. The clone and detailed information can be
 obtained from Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES	source	Location/Qualifiers
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		/mol_type="genomic DNA"
		/db_xref="taxon:10090"
		/chromosome="18"
		/map="18"
		/clone="RP24-243L15"
		/clone_lib="RPCI-24"
repeat_region	1629..1683	/rpt_family="L1"
repeat_region	3465..3530	/rpt_family="MIR"
repeat_region	3709..3767	/rpt_family="MER1_type"
repeat_region	3768..4484	/rpt_family="RMR6A"
repeat_region	4493..4545	/rpt_family="B4"
repeat_region	6368..6897	/rpt_family="ERV1"
repeat_region	7286..7388	/rpt_family="MaLR"
repeat_region	7625..7848	/rpt_family="RMR6A"
repeat_region	7978..8124	/rpt_family="Alu"
repeat_region	8127..8519	/rpt_family="RMR6A"
repeat_region	8525..8668	/rpt_family="Alu"
repeat_region	8742..9568	/rpt_family="RMR19A"
repeat_region	9569..9649	/rpt_family="RMR6A"
repeat_region	9655..10034	/rpt_family="L1"
repeat_region	10065..10342	/rpt_family="ERVK"
repeat_region	10585..10634	/rpt_family="RMR6A"
repeat_region	10663..10852	/rpt_family="RAL_RN"
repeat_region	10695..11211	/rpt_family="ERV1"
repeat_region	11212..11264	/rpt_family="ERV1"
repeat_region	11284..11521	/rpt_family="ERV1"
repeat_region	12965..13010	/rpt_family="B4"
repeat_region	13012..13075	/rpt_family="ERV1"
repeat_region	13348..13618	/rpt_family="ERV1"
repeat_region	14328..14663	/rpt_family="ERV1"
repeat_region	14665..14713	/rpt_family="tRNA-Arg-AGG"
repeat_region	14716..14867	


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repeat_region /rpt_family="ERV1"
repeat_region 15462..15953
repeat_region /rpt_family="RMR6A"
repeat_region 16095..16172
repeat_region /rpt_family="Alu"
repeat_region 16295..16477
repeat_region /rpt_family="B2"
repeat_region 16743..16827
repeat_region /rpt_family="ERV1"
repeat_region 16836..17256
repeat_region /rpt_family="ERVK"
repeat_region 18595..18691
repeat_region /rpt_family="B4"
repeat_region 18776..18922
repeat_region /rpt_family="Alu"
repeat_region 20784..20974
repeat_region /rpt_family="B2"
repeat_region 21648..21835
repeat_region /rpt_family="B2"
repeat_region 21846..21973
repeat_region /rpt_family="Alu"
repeat_region 23208..23348
repeat_region /rpt_family="Alu"
misc_feature 24837..24910
repeat_region /notes="Sequence derived from PCR product of project DNA."
repeat_region 25025..25233
repeat_region /rpt_family="L1"
unsure 25075..25085
repeat_region /note="Sequence derived from one plasmid subclone."
repeat_region 25469..25619
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repeat_region 25622..25734
repeat_region /rpt_family="L1"
repeat_region 25769..25929
repeat_region /rpt_family="B4"
repeat_region 26971..27138
repeat_region /rpt_family="ERV1"
repeat_region 27706..27873
repeat_region /rpt_family="B2"
repeat_region 27874..28022
repeat_region /rpt_family="Alu"
repeat_region 28023..28066
repeat_region /rpt_family="B2"
repeat_region 28362..28381
repeat_region /rpt_family="B2"
repeat_region 28382..28531
repeat_region /rpt_family="Alu"
repeat_region 28532..28700
repeat_region /rpt_family="B2"
repeat_region 29417..29766
repeat_region /rpt_family="MaLR"
repeat_region 31583..31941
repeat_region /rpt_family="MaLR"
repeat_region 32560..32657
repeat_region /rpt_family="MaLR"
repeat_region 32658..32798
repeat_region /rpt_family="Alu"
repeat_region 32944..33341
repeat_region /rpt_family="ERVK"
repeat_region 34057..34154
repeat_region /rpt_family="Alu"
repeat_region 34077..34168
repeat_region /rpt_family="B4"

Query Match 12.9%; Score 165.4; DB 10; Length 160728;
Best Local Similarity 91.6%; Pred. No. 1.3e-37;
Matches 175; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTTAC 189
Db 22728 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCATGGCCAGCCAGACTGTATCATTTAC 22669
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QY 190 GTGTGATGGCAACAACATCACCGGTCAAAACCCGAGAGACAGTGAAGACGACTGTGTCTC 249
Db 22668 GTGTGATGGCAACAACATCACCGGTCAAAACCTGAGAGCAGTGAAGACCAACCGTGTCTC 22609
QY 250 TTGTAACTCTGGGAGAGAACTTTTGTATGAAACGACAGCTGATGGCAGAAACTCAGGTTCAG 309
Db 22608 TTGTAACTCTGGGAGAGAACTTTTGTATGAAACGACAGCTGATGGCAGAAACTCAGGTTCAG 22549
QY 310 CTACACATAC 320
Db 22548 CTGCACCTTCC 22538

AC147992 239075 bp DNA linear ROD 10-JUL-2004
Mus musculus BAC clone RP24-384K8 from chromosome 18, complete
sequence.
AC147992
VERSION AC147992.3 GI:49170304
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Tomlinson, C., Bielicki, L. and Meyer, R.
The sequence of Mus musculus BAC clone RP24-384K8
Unpublished (2001)
REFERENCE 3 (bases 1 to 239075)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 239075)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 239075)
AUTHORS Wilson, R.K.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2004) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 24, 2004 this sequence version replaced gi:47131351.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics
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Center project name: M_BB0384K08
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NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,

Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC147367.

FEATURES

Location/Qualifiers

source

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repeat_region
1673..1711
/rpt_family="L1"
repeat_region
1712..1894
/rpt_family="B2"
repeat_region
1895..1925
/rpt_family="L1"
repeat_region
1959..1986
/rpt_family="L2"
repeat_region
2031..2099
/rpt_family="ID"
repeat_region
2129..2282
/rpt_family="B4"
repeat_region
4012..4049
/rpt_family="MIR"
repeat_region
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37337..37436
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38114..38246
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48740..48962
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50844..50972
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51687..51756
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52340..52434
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52647..52744
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52740..52808
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Query Match 12.9%; Score 165.4; DB 10; Length 239075;
Best Local Similarity 91.6%; Pred. No. 1.4e-37;

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Matches 175; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 189
Db 218789 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 218848
QY 190 GTGTGATGGCAACAACATCAGCGTCAAAACCGAGGACGACAGTGAAGACGACTGTGTTCTC 249
Db 218849 GTGTGATGGCAACAACATCAGCGTCAAAACCGAGGACGACAGTGAAGACGACTGTGTTCTC 218908
QY 250 TTGTAACTCTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAGAAAACCTGAGTTCAG 309
Db 218909 TTGTAACTCTGGGAGAGAGCTTTGTATGAACGACAGCTGTATGGCAGAGAAAACCTGAGTTCAG 218968
QY 310 CTACAACATAC 320
Db 218969 CTGACACTTCC 218979

RESULT 14
AL954662/c
LOCUS
DEFINITION
  Mouse DNA sequence from clone RP23-348L16 on chromosome 2, complete
  sequence.
ACCESSION
  AL954662
VERSION
  AL954662.13 GI:37718670
KEYWORDS
  HTG.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Brown, J.
  Direct Submission
  Submitted (17-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
  humquery@sanger.ac.uk
  On Oct 17, 2003 this sequence version replaced gi:33666998.
  Sequence from the Mouse Genome Sequencing Consortium whole genome
  shotgun may have been used to confirm this sequence. Sequence data
  from the whole genome shotgun align has only been used where it has
  a phred quality of at least 30.
  ----- Genome Center
  Center: Wellcome Trust Sanger Institute
  Center code: SC
  Web site: http://www.sanger.ac.uk
  Contact: humquery@sanger.ac.uk
  -----
  During sequence assembly data is compared from overlapping clones.
  Where differences are found these are annotated as variations
  together with a note of the overlapping clone name. Note that the
  variation annotation may not be found in the sequence submission
  corresponding to the overlapping clone, as we submit sequences with
  only a small overlap as described above.
  This sequence was finished as follows unless otherwise noted: all
  regions were either double-stranded or sequenced with an alternate
  chemistry or covered by high quality data (i.e., phred quality >=
  30); an attempt was made to resolve all sequencing problems, such
  as compressions and repeats; all regions were covered by at least
  one plasmid subclone or more than one M13 subclone; and the
  assembly was confirmed by restriction digest, except on the rare
  occasion of the clone being a YAC.
  The following abbreviations are used to associate primary accession
  numbers given in the feature table with their source databases:
  Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
  on the WORMPEP database can be found at
  http://www.sanger.ac.uk/Projects/C_elegans/wormpep/RP23-348L16 is
  from the RPI-23 Mouse BAC Library
  constructed by the group of Pieter de Jong.
  For further details see http://www.chori.org/bacpac/home.htm
  VECTOR: pBACE3.6.
  Location/Qualifiers
    1..132427

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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosomes="2"
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/clone_lib="RPI-23"

ORIGIN

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Best Local Similarity 92.1%; Pred. No. 1.7e-37;
Matches 174; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 189
Db 14768 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 14709
QY 190 GTGTGATGGCAACAACATCAGCGTCAAAACCGAGGACGACAGTGAAGACGACTGTGTTCTC 249
Db 14708 GTGTGATGGCAACAACATCAGCGTCAAAACCGAGGACGACAGTGAAGACGACTGTGTTCTC 14649
QY 250 TTGTAACTCTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAGAAAACCTGAGTTCAG 309
Db 14648 TTGTAACTCTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAGAAAACCTGAGTTCAG 14589
QY 310 CTACAACAT 318
Db 14588 CTGACACTT 14580

RESULT 15
AL954662/c
LOCUS
DEFINITION
  Mus musculus BAC clone RP24-152G20 from chromosome 18, complete
  sequence.
ACCESSION
  AC139157
VERSION
  AC139157.4 GI:40288242
KEYWORDS
  HTG.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Swearingen-Shahid, S., Shahid, S., Kozlowicz, A., Bielicki, L. and
  Meyer, R.
  The sequence of Mus musculus BAC clone RP24-152G20
  Unpublished (2001)
  2 (bases 1 to 133869)
  Wilson, R.
  Sequencing of Mus musculus
  Unpublished (2001)
  3 (bases 1 to 133869)
  McPherson, J.D. and Waterston, R.H.
  Direct Submission
  Submitted (24-JAN-2003) Genome Sequencing Center, 4444 Forest Park
  Parkway, St. Louis, MO 63108, USA
  4 (bases 1 to 133869)
  Wilson, R.K.
  Direct Submission
  Submitted (24-SEP-2003) Genome Sequencing Center, 4444 Forest Park
  Parkway, St. Louis, MO 63108, USA
  5 (bases 1 to 133869)
  Wilson, R.K.
  Direct Submission
  Submitted (22-DEC-2003) Genome Sequencing Center, 4444 Forest Park
  Parkway, St. Louis, MO 63108, USA
  6 (bases 1 to 133869)
  Wilson, R.
  Direct Submission
  Submitted (01-JAN-2004) Department of Genetics, Washington
  University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
  On Dec 22, 2003 this sequence version replaced gi:35069405.
  ----- Genome Center
  Center: Washington University Genome Sequencing Center

```

FEATURES
source

Center code: WUGSC
 Web site: <http://genome.wustl.edu>
 Contact: submissions@watson.wustl.edu
 ----- Summary Statistics -----
 Center project name: M_BB0152G20

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC130218.

FEATURES

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   /note="Unresolved simple sequence repeat."
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   /note="Unresolved simple sequence repeat."
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   /note="Unresolved tandem repeat."
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   /note="CpG island (%GC=71.2, o/e=0.74, #CpGs=97)"
133392..133869
   /note="Unresolved tandem repeat."

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ORIGIN

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Query Match      12.7%; Score 162.2; DB 10; Length 133869;
Best Local Similarity 90.6%; Pred. No. 1.2e-36;
Matches 173; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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DB 86505 AGGAGTAGACTGGCTCTTAGGAGATGGCTGCCATGGCCAGCTGATCATTTAT 86564
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QY 190 GTGTGATGTCACCAACATCACCGTCAAAACCCAGAGACAGTGAAGACGACTGTGTTCTC 249
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QY 310 CTACAAACATAC 320
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 DB 86685 CTGCACCTTCC 86695

Search completed: July 12, 2005, 17:41:12
 Job time : 5913.77 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 18:01:50 ; Search time 5881.03 Seconds
(without alignments)
8878.154 Million cell updates/sec

Title: US-09-788-074-2

Perfect score: 1279

Sequence: 1 aatgggagcaacatgctagc.....tctatgagaagtgcattga 1279

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 45554873 seqs, 20411521753 residues

Total number of hits satisfying chosen parameters: 91109746

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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96: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
97: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
98: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
99: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
100: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
101: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
102: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
103: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
104: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
105: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
106: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
107: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
108: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
109: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
110: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
111: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
112: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
113: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
114: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
115: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*
116: /cgn2_6/ptodata/1/pna/US0999P_COMB.seq.*

Db 721 GGAAGATGATCGTGGTGAGCATCAAGCACTGGCACCATGCTGGGATTGGCGCTGCAGCC 780
Qy 781 ACAGTTGTCTAATCAACCACTTGGGTCAATGGTCTTTTAAACAAGAGAAAGAACTTAGGAGG 840
Db 781 ACAGTTGTCTAATCAACCACTTGGGTCAATGGTCTTTTAAACAAGAGAAAGAACTTAGGAGG 840
Qy 841 ACAATCTGAAATACCAAGTTAGAAACGAGAGTCTCTATTCTGAGGCGAGCCCTTGTGG 900
Db 841 ACAATCTGAAATACCAAGTTAGAAACGAGAGTCTCTATTCTGAGGCGAGCCCTTGTGG 900
Qy 901 GGACGGAGAGTGAATGGGATCCAGGATGCTGGCTGCAGCAGAGCCCTGAGAGCTGGCAGGC 960
Db 901 GGACGGAGAGTGAATGGGATCCAGGATGCTGGCTGCAGCAGAGCCCTGAGAGCTGGCAGGC 960
Qy 961 CACCGAGCAGCCCTCTCTCGGTACATTTGAATTTAAGTAAGGATATTTGCGCAAAACACATG 1020
Db 961 CACCGAGCAGCCCTCTCTCGGTACATTTGAATTTAAGTAAGGATATTTGCGCAAAACACATG 1020
Qy 1021 AATAATTTAGATCATATCCAGTCTTTAGTCTGCAGGCGCAGCAATATACATATAAC 1080
Db 1021 AATAATTTAGATCATATCCAGTCTTTAGTCTGCAGGCGCAGCAATATACATATAAC 1080
Qy 1081 AAAACAGCAGCTCTAGTCTCTTGGATTTGAATCTGAGATGTTGTTTCTGTTAGGT 1140
Db 1081 AAAACAGCAGCTCTAGTCTCTTGGATTTGAATCTGAGATGTTGTTTCTGTTAGGT 1140
Qy 1141 TGGTTACAGCGCTTTATAGATTTGCCCAACACATCTCTGAAATGACAGTTGGCC 1200
Db 1141 TGGTTACAGCGCTTTATAGATTTGCCCAACACATCTCTGAAATGACAGTTGGCC 1200
Qy 1201 TGAGACTCTATCTTCTCTAGGAGTGTGTCATGAACATGCCACCTGCACCTGGGT 1260
Db 1201 TGAGACTCTATCTTCTCTAGGAGTGTGTCATGAACATGCCACCTGCACCTGGGT 1260
Qy 1261 CTATGAGAGGTGCAATGA 1279
Db 1261 CTATGAGAGGTGCAATGA 1279

RESULT 2

US-60-466-412-85481

; Sequence 85481, Application US/60466412

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele

; APPLICANT: IAKOUBOVA, Olga

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001466

; CURRENT APPLICATION NUMBER: US/60/466,412

; CURRENT FILING DATE: 2003-04-30

; NUMBER OF SEQ ID NOS: 429241

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 85481

; LENGTH: 16239

; TYPE: DNA

; ORGANISM: Homo sapiens

US-60-466-412-85481

Query Match

Best Local Similarity 59.2%; Pred. No. 7,4e-76; Length 16239;

Matches 720; Conservative 2; Mismatches 424; Indels 70; Gaps 10;

Qy 126 CCACAGGAGTAGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGAGCTGTATCA 185
Db 8820 CTACAGGAGTGGGAATAGCTTTGCGAATAATGGCGCAATGGCCAGCCAGATGTATCA 8879
Qy 186 TTACGTGTGATGGCAACACATCAGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGT 245
Db 8880 TCACCTTGTGATGTTAAAAACCTCACCATAAAAACTGAGAGCACCTTTGAAAAACAACACATG 8939
Qy 246 TCTCTTGTAACTCGGAGAGAGTTTGTGAACGACGACTGTATGCGAGAAAACTGAGG 305
Db 8940 TTTCTTGTACCTCGGAGAGAGTTTGAAGAAACACACGCTGTATGCGAGAAAACTCAGG 8999

RESULT 3

US-09-724-676-2658

; Sequence 2658, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2658
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2658

```
Query Match          17.1%; Score 218.4; DB 33; Length 838;
Best Local Similarity 61.2%; Pred. No. 3.5e-53;
Matches 427; Conservative 0; Mismatches 256; Indels 15; Gaps 4;

QY 130 AGGAGTGGAGCTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db 131 AGGAGTGGGAATAGCTTTTCGAAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 190

QY 190 GTGTGATGGCAACATCACCGTCAAAACCCGAGAGCAGCTGAAGACGACTGTGTCTC 249
Db 191 TTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACTTTGAAAAACAACACAGTTTC 250

QY 250 TTGTAACTCTGGGAGAGAAAGTTTGAATGAAACGACAGCTGATGCGAGAAAAAAGTGGTTCAG 309
Db 251 TTGTACCTCTGGGAGAGAAAGTTTGAAGAAACACAGCTGATGCGAGAAAAAAGTCCGGTCCA 310

QY 310 CTACAACTACTGTGAAGCGACAGAGCTTCTAGATTTTACAGATTAATTTGCAATTAACAA 369
Db 311 GTCGTGACCATGTTATGAATCAGAAAGCTTCTGAATGATAGGCTGTAT----CAATAAC 366

QY 370 TGTCTGTACTTACTGCCAGGCTGACTGAAAAAAGTCTTATGAGAGTTGACTTTTGAT 429
Db 367 ATTTTACTGTTTATAGGCAGAACTTAATGAAAAAGTTATTTTAT--GAATTGAATTTTGTG 425

QY 430 AAATAGTAAAAAGTCCCGAGCTTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAA 489
Db 426 AAATAGCAAAAGTATCAACTTCATCAGAAATTTGAGTCTTTTATAGTACTAGGTTG 485

QY 490 AGCAGATAGTTGTTATTTGTAACAAATCAGATATGATGGGTGGAGT----TCAGAGAGG 545
Db 486 AAACCCACAACTATTTGTAATTAATCAATATGGGTTAATGAAGTAGACTCAGAAAGGA 545

QY 546 AAAGCGAAGACTTGTGGAGT-----GGTGTGGGTCTCTGGGGTTCCTTCACTTTGA 599
Db 546 GAAGGTGAAACAAATGTTGATTAAGGAGGTTATGAGTCATGGAACCTCTTGTAAATGTACT 605

QY 600 AGATGATGAACCTAACCTACCTGTATTTTTCGAGAGGCTGACCTTCCAGACGGTGCC 659
Db 606 TGAAGATTAACACGTTTACTTTGTTTTCGAGACTGTCTGCACCTTTACAGATGGTGA 665

QY 660 CTGGTCCAGCACAGCAATGGGACGGGAGGAGACAGATAAACAAGAAAACTGAAGGAT 719
Db 666 TTGGTTTACGATCAGAGGTGGGATGGGAGGAAAGACACAATTAACAGAAAAATGAAGAT 725

QY 720 GGGAGATGATCGTGGTGAAGCATCAAGCATCAAGCATGGGACCATGCTGGGATTTGGCCCTGCAGC 779
Db 726 GGGAAATAGTGGTGAAGTGTCAAACTGCTGTCTCAGTCAGCTTCTTGTGTGCATT 785

QY 780 CACAGTTGTCAACCACTTCGGGTCAATTTGGTTCCTTTA 817
Db 786 CATAGTTTCACTAATCTTCTATATCATTTGATCAATTA 823
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RESULT 4

US-09-724-676A-2658

; Sequence 2657, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD

RESULT 5

US-09-724-676-2657

; Sequence 2658, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2658
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2658

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Query Match          17.1%; Score 218.4; DB 33; Length 838;
Best Local Similarity 61.2%; Pred. No. 3.5e-53;
Matches 427; Conservative 0; Mismatches 256; Indels 15; Gaps 4;

QY 130 AGGAGTGGAGCTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db 131 AGGAGTGGGAATAGCTTTTCGAAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 190

QY 190 GTGTGATGGCAACATCACCGTCAAAACCCGAGAGCAGCTGAAGACGACTGTGTCTC 249
Db 191 TTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACTTTGAAAAACAACACAGTTTC 250

QY 250 TTGTAACTCTGGGAGAGAAAGTTTGAATGAAACGACAGCTGATGCGAGAAAAAAGTGGTTCAG 309
Db 251 TTGTACCTCTGGGAGAGAAAGTTTGAAGAAACCAACAGCTGATGCGAGAAAAAAGTCCGGTCCA 310

QY 310 CTACAACTACTGTGAAGCGACAGAGCTTCTAGATTTTACAGATTAATTTGCAATTAACAA 369
Db 311 GTCGTGACCATGTTATGAATCAGAAAGCTTCTGAATGATAGGCTGTAT----CAATAAC 366

QY 370 TGTCTGTACTTACTGCCAGGCTGACTGAAAAAAGTCTTATGAGAGTTGACTTTTGAT 429
Db 367 ATTTTACTGTTTATAGGCAGAACTTAATGAAAAAGTTATTTTAT--GAATTGAATTTTGTG 425

QY 430 AAATAGTAAAAAGTCCCGAGCTTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAA 489
Db 426 AAATAGCAAAAGTATCAACTTCATCAGAAATTTGAGTCTTTTATAGTACTAGGTTG 485

QY 490 AGCAGATAGTTGTTATTTGTAACAAATCAGATATGATGGGTGGAGT----TCAGAGAGG 545
Db 486 AAACCCACAACTATTTGTAATTAATCAATATGGGTTAATGAAGTAGACTCAGAAAGGA 545

QY 546 AAAGCGAAGACTTGTGGAGT-----GGTGTGGGTCTCTGGGGTTCCTTCACTTTGA 599
Db 546 GAAGGTGAAACAAATGTTGATTAAGGAGGTTATGAGTCATGGAACCTCTTGTAAATGTACT 605

QY 600 AGATGATGAACCTAACCTACCTGTATTTTTCGAGAGGCTGACCTTCCAGACGGTGCC 659
Db 606 TGAAGATTAACACGTTTACTTTGTTTTCGAGACTGTCTGCACCTTTACAGATGGTGA 665

QY 660 CTGGTCCAGCACAGCAATGGGACGGGAGGAGACAGATAAACAAGAAAACTGAAGGAT 719
Db 666 TTGGTTTACGATCAGAGGTGGGATGGGAGGAAAGACACAATTAACAGAAAAATGAAGAT 725

QY 720 GGGAGATGATCGTGGTGAAGCATCAAGCATCAAGCATGGGACCATGCTGGGATTTGGCCCTGCAGC 779
Db 726 GGGAAATAGTGGTGAAGTGTCAAACTGCTGTCTCAGTCAGCTTCTTGTGTGCATT 785

QY 780 CACAGTTGTCAACCACTTCGGGTCAATTTGGTTCCTTTA 817
Db 786 CATAGTTTCACTAATCTTCTATATCATTTGATCAATTA 823
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; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2657
; LENGTH: 1105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2657

Query Match 15.7%; Score 201.4; DB 33; Length 1105;
Best Local Similarity 62.2%; Pred. No. 4.8e-48;
Matches 389; Conservative 0; Mismatches 221; Indels 15; Gaps 4;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGAGCTGTATCATTTAC 189
DB 131 AGGAGTGGGAATAGCTTTGCGAATAATGGCGCAATGGCCAGCCAGATTTGTATCATCAC 190
QY 190 GTGTGATGGCAACAACATCACCGGTCAAAACCCGAGAGCAGCTGAGACGACCTGTGTCTC 249
DB 191 TTGTGATGTTAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACACAGTTTTC 250
QY 250 TTGTAACCTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAGAAAACTGAGGTGAG 309
DB 251 TTGTACCTGGGAGAGAGTTTGAAGAAACCAAGCTGATGGCAGAAAACTCCGGTCCA 310
QY 310 CTACAACATCTGTGGAAGCGACAGAGCTTCTAGATTTACAGATTAATTTGCAATTAACA 369
DB 311 GTGCTGACCATGTTATGAATCACGAGCTTCTGAATGATAGCTGTAT----CAATAAC 366
QY 370 TGTCTGTACTTACTGCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGAT 429
DB 367 ATTTTACTGTTTATAGGCAGAACTTAATGAAAAAGTTATTTAT--GAATTTGAATTTGTC 425
QY 430 AAATTAGTAAAGTCCAGAGCTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAA 489
DB 426 AAATTAGCAAAAGTATCAACTTTCATCATAAGATTGGCATCTTTTATTTAGCTACTAGGTTG 485
QY 490 AGCACAATGTTGTTGCAACAAATCAGATGATGGGGTGGAGT---TCAGAGAGGG 545
DB 486 AAAACCAACAACCTATTGTGAATAAATCAATATGGGTTAATGAAGTAGACTCAGAAAGGA 545
QY 546 AAAGCGAAGACTGTTTGGAGT-----GGTGTGGGTCTCTGGGGTTCCTTCACTTTGGA 599
DB 546 GAAGGTGAAACAAATGTTGATTAAAGGAGTTATGAGTCATGGAACCTTTGTAATGTACT 605
QY 600 AGATGATGAACCTAACTACCTCTGTTATTTTGGCAGCGGTCTGCACCTTCCAGACGGTGCC 659
DB 606 TCGAAGATTAAACCGTTTACTTTGTTTGGCAGACTGTCTGCAACTTTACAGATGGTGCA 665
QY 660 CTGGTCCAGCAGCAATGGGACGGGAGGAGAGCAGCATTAACAGAAAACTGAAGGAT 719
DB 666 TTGGTTTCAGCATCAGAGTGGGATGGGAAGGAAGCAATTAACAGAAAAATTTGAAGAT 725
QY 720 GGGAAAGATGATCGTGTGAGCATCA 744
DB 726 GGGAAATTAGTGGTGGAGTGTGTCA 750

RESULT 6

US-09-724-676A-2657
; Sequence 2657, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2657

; LENGTH: 1105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2657

Query Match 15.7%; Score 201.4; DB 33; Length 1105;
Best Local Similarity 62.2%; Pred. No. 4.8e-48;
Matches 389; Conservative 0; Mismatches 221; Indels 15; Gaps 4;
QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGAGCTGTATCATTTAC 189
DB 131 AGGAGTGGGAATAGCTTTGCGAATAATGGCGCAATGGCCAGCCAGATTTGTATCATCAC 190
QY 190 GTGTGATGGCAACAACATCACCGGTCAAAACCCGAGAGCAGCTGAGACGACCTGTGTCTC 249
DB 191 TTGTGATGTTAAACCTCACCATATAAACTGAGAGCACTTTGAAAAACAACACAGTTTTC 250
QY 250 TTGTAACCTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAGAAAACTGAGGTGAG 309
DB 251 TTGTACCTGGGAGAGAGTTTGAAGAAACCAAGCTGATGGCAGAAAACTCCGGTCCA 310
QY 310 CTACAACATCTGTGGAAGCGACAGAGCTTCTAGATTTACAGATTAATTTGCAATTAACA 369
DB 311 GTGCTGACCATGTTATGAATCACGAGCTTCTGAATGATAGCTGTAT----CAATAAC 366
QY 370 TGTCTGTACTTACTGCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGAT 429
DB 367 ATTTTACTGTTTATAGGCAGAACTTAATGAAAAAGTTATTTAT--GAATTTGAATTTGTC 425
QY 430 AAATTAGTAAAGTCCAGAGCTAAGAAATGAAGACATCTTATGAGTTCTAGATCGAAA 489
DB 426 AAATTAGCAAAAGTATCAACTTTCATCATAAGATTGGCATCTTTTATTTAGCTACTAGGTTG 485
QY 490 AGCACAATGTTGTTGCAACAAATCAGATGATGGGGTGGAGT---TCAGAGAGGG 545
DB 486 AAAACCAACAACCTATTGTGAATAAATCAATATGGGTTAATGAAGTAGACTCAGAAAGGA 545
QY 546 AAAGCGAAGACTGTTTGGAGT-----GGTGTGGGTCTCTGGGGTTCCTTCACTTTGGA 599
DB 546 GAAGGTGAAACAAATGTTGATTAAAGGAGTTATGAGTCATGGAACCTTTGTAATGTACT 605
QY 600 AGATGATGAACCTAACTACCTCTGTTATTTTGGCAGCGGTCTGCACCTTCCAGACGGTGCC 659
DB 606 TCGAAGATTAAACCGTTTACTTTGTTTGGCAGACTGTCTGCAACTTTACAGATGGTGCA 665
QY 660 CTGGTCCAGCAGCAATGGGACGGGAGGAGAGCAGCATTAACAGAAAACTGAAGGAT 719
DB 666 TTGGTTTCAGCATCAGAGTGGGATGGGAAGGAAGCAATTAACAGAAAAATTTGAAGAT 725
QY 720 GGGAAAGATGATCGTGTGAGCATCA 744
DB 726 GGGAAATTAGTGGTGGAGTGTGTCA 750

RESULT 7

US-09-724-676-2656
; Sequence 2656, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2656
; LENGTH: 1369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676-2656
Query Match 15.7%; Score 201.4; DB 33; Length 1369;
Best Local Similarity 62.2%; Pred. No. 5.4e-48;

Matches 389; Conservative 0; Mismatches 221; Indels 15; Gaps 4;
QY 130 AGGAGTAGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACGTGTATCATTTAC 189
|||||
Db 131 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTTGTATCATCAC 190
|||||
QY 190 GTGTGATGGCAACAATCATCCGCTCAAAACCCGAGAGCAGTGAAGAGCAGCTGTCTCTC 249
|||||
Db 191 TTGTGATGTAATAAACCTCACCATAAATCTGAGAGCACTTTGAAAAACAACACAGTTTTTC 250
|||||
QY 250 TTGTAACTCTGGAGAGAGTTTGTATGAACACGACGTGATGGCAGAAAAAACTGAGGTGAG 309
|||||
Db 251 TTGTACCTCTGGAGAGAGTTTGAAGAACACACAGCTGATGGCAGAAAAAACTCCGGTCCA 310
|||||
QY 310 CTACAACTACTGTGAAGCGGACAGAAGCTTCTAGATTTTACAGATTAATGCAATTAACAA 369
|||||
Db 311 GTGTGACCATGTTATGAATCAGGAAGCTTCTGAATGATAGGCTGTAT----CAATAAC 366
|||||
QY 370 TGTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTTTGAT 429
|||||
Db 367 ATTTTACTGTTTATAGGCGAAGCTTAATGAAAAAGTTATTTTAT--GAATTGAATTTTCTC 425
|||||
QY 430 AAATAGTAAAGTCCCGAGCACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAA 489
|||||
Db 426 AAATAGCAAAAGTATCAACTTTCATCATAGATTGCGCATCTTTTATAGCTACTAGGTTG 485
|||||
QY 490 AGCAGATAGTTGTTTGAACAAATCAGTATGATGGGTGGAGT----TCAGAGAGGG 545
|||||
Db 486 AAAACCACAAACTATTGTGAATAAATCAATATGGGTTAATGAAGTAGACTCAGAAGGA 545
|||||
QY 546 AAAGCGAGACTTGTGGAGT-----GGTGTGGGTCTGGGGTTCCTTCACITTTGA 599
|||||
Db 546 GAAGGTGAACAAATGTTGATTAAAGAGGTTATGAGTCAATGAAAACTCTTGTATGTACT 605
|||||
QY 600 AGATGATGAATTAACCTGATCCCTGATTTTTCAGACGGTCTGCACCTTCCAGACGGTGCC 659
|||||
Db 606 TGGAGATTAAACGTTTACTTTGTTTTCAGACTGCTGCACTTTACAGATGGTGA 665
|||||
QY 660 CTGGTCCAGCACAGCAATGGGCGGAAGGAGAGCAGATTAACAGAAAACTGAAGAT 719
|||||
Db 666 TTGGTTTCAGCATCAGGAGTGGGATGGGAAGGAAAGCACAATAACAGAAAAATTGAAGAT 725
|||||
QY 720 GGGAGATGATCGTGTGAGCATCA 744
|||||
Db 726 GGGAAATTAGTGGTGGAGTGTGCA 750
|||||

RESULT 8

US-09-724-676A-2656
; Sequence 2656, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2656
; LENGTH: 1369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-724-676A-2656

Query Match 15.7%; Score 201.4; DB 33; Length 1369;
Best Local Similarity 62.2%; Pred. No. 5.4e-48;
Matches 389; Conservative 0; Mismatches 221; Indels 15; Gaps 4;
QY 130 AGGAGTAGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACGTGTATCATTTAC 189
|||||
Db 131 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTTGTATCATCAC 190
|||||
QY 190 GTGTGATGGCAACAATCATCCGCTCAAAACCCGAGAGCAGTGAAGAGCAGCTGTCTCTC 249
|||||

Db 191 TTGTGATGGTAAAAAACCCTCACCATAAAAAATGAGAGCACTTTTGAAAAAACAACACAGTTTTTC 250
|||||
QY 250 TTGTAACTCTGGAGAGAGTTTGTATGAATAACGACAGCTGATGGCAGAAAAAACTGAGGTGAG 309
|||||
Db 251 TTGTACCTCTGGAGAGAGTTTGAAGAACACACAGCTGATGGCAGAAAAAACTCCGGTCCA 310
|||||
QY 310 CTACAACTACTGTGAAGCGGACAGAAGCTTCTAGATTTTACAGATTAATGCAATTAACAA 369
|||||
Db 311 GTGTGACCATGTTATGAATCAGGAAGCTTCTGAATGATAGGCTGTAT----CAATAAC 366
|||||
QY 370 TGTCTGTACTTACTGCCAAGGCTGACTGAAAAAACTACTTTTATGGAGTTGACTTTTGAT 429
|||||
Db 367 ATTTTACTGTTTATAGGCGAAGCTTAATGAAAAAGTTATTTTAT--GAATTGAATTTTCTC 425
|||||
QY 430 AAATAGTAAAGTCCCGAGCACTAAGAAATGAAGACATCTTATGAGTTTCTAGATCGAAA 489
|||||
Db 426 AAATAGCAAAAGTATCAACTTTCATCATAGATTGCGCATCTTTTATAGCTACTAGGTTG 485
|||||
QY 490 AGCAGATAGTTGTTTGAACAAATCAGTATGATGGGTGGAGT----TCAGAGAGGG 545
|||||
Db 486 AAAACCACAAACTATTGTGAATAAATCAATATGGGTTAATGAAGTAGACTCAGAAGGA 545
|||||
QY 546 AAAGCGAGACTTGTGGAGT-----GGTGTGGGTCTGGGGTTCCTTCACITTTGA 599
|||||
Db 546 GAAGGTGAACAAATGTTGATTAAAGAGGTTATGAGTCAATGAAAACTCTTGTATGTACT 605
|||||
QY 600 AGATGATGAATTAACCTGATCCCTGATTTTTCAGACGGTCTGCACCTTCCAGACGGTGCC 659
|||||
Db 606 TGGAGATTAAACGTTTACTTTGTTTTCAGACTGCTGCACTTTACAGATGGTGA 665
|||||
QY 660 CTGGTCCAGCACAGCAATGGGCGGAAGGAGAGCAGATTAACAGAAAACTGAAGAT 719
|||||
Db 666 TTGGTTTCAGCATCAGGAGTGGGATGGGAAGGAAAGCACAATAACAGAAAAATTGAAGAT 725
|||||
QY 720 GGGAGATGATCGTGTGAGCATCA 744
|||||
Db 726 GGGAAATTAGTGGTGGAGTGTGCA 750
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RESULT 9

US-10-631-467-1237
; Sequence 1237, Application US/10631467
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1237
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-631-467-1237

Query Match 13.8%; Score 176.6; DB 58; Length 933;
Best Local Similarity 95.3%; Pred. No. 1.1e-40;
Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 130 AGGAGTAGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACGTGTATCATTTAC 189
|||||
Db 112 AGGAGTAGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACGTGTATCATTTAC 171
|||||
QY 190 GTGTGATGGCAACAATCATCCGCTCAAAACCCGAGAGCAGTGAAGAGCAGCTGTCTCTC 249
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Db 172 GTGTGATGGCAACAATCATCCGCTCAAAACCCGAGAGCAGTGAAGAGCAGCTGTCTCTC 231
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QY 250 TTGTAACCTGGAGAGAGTTTGTATGAACAGCAGCTGATGCGAGAGAACTGAGGTGAG 309
DB 232 TTGTAACCTGGAGAGAGTTTGTATGAACAGCAGCTGATGCGAGAGAACTGAGACGGT 291
QY 310 CTACACATAC 320
DB 292 CTGACCTTCC 302

RESULT 10

US-10-764-420-1507
; Sequence 1507, Application US/10764420
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent
; TITLE OF INVENTION: Possesses A Defined Biological Activity
; FILE REFERENCE: ROS122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1507
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-1507

Query Match 13.8%; Score 176.6; DB 62; Length 933;
Best Local Similarity 95.3%; Pred. No. 1.1e-40;
Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 189
DB 112 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 171
QY 190 GTGTGATGCGACATCATCAGCTCAAAACCGAGAGCAGCTGAGAGCGACTGTCTTC 249
DB 172 GTGTGATGCGACATCATCAGCTCAAAACCGAGAGCAGCTGAGAGCGACTGTCTTC 231
QY 250 TTGTAACCTGGAGAGAGTTTGTATGAACAGCAGCTGATGCGAGAGAACTGAGGTGAG 309
DB 232 TTGTAACCTGGAGAGAGTTTGTATGAACAGCAGCTGATGCGAGAGAACTGAGACGGT 291
QY 310 CTACACATAC 320
DB 292 CTGACCTTCC 302

RESULT 11

US-10-029-386-5224
; Sequence 5224, Application US/10029386
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5224
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:

; OTHER INFORMATION: MAP TO AF181449.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EST HUMAN HIT: AA428498.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q01469, EVALUATE 1.00e-27
; OTHER INFORMATION: NT HIT: g113642859, EVALUATE 2.00e-93
US-10-029-386-5224

Query Match 13.7%; Score 175.6; DB 46; Length 537;
Best Local Similarity 67.6%; Pred. No. 1.6e-40;
Matches 277; Conservative 0; Mismatches 129; Indels 4; Gaps 2;
QY 126 CCACAGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCA 185
DB 98 CTACAGGAGTGGGAATAGCTTTGCCGAAATAATGGGCGCAATGGCCAGCAGATTGTATCA 157
QY 186 TTACGTGTATGGGCAACACATCAGGCTCAAAACCGAGAGCAGCTGAGACGACTGTCT 245
DB 158 TCACCTGTGTATGGTAAACACCTCACCATAAAACCTTGAGAGCAGCTTTGAAAAACAACAGT 217
QY 246 TCTCTTGTAACTGGGAGAGAGTTTGTATGAACAGCAGCTGATGCGAGAGAACTGAGG 305
DB 218 TTTCTTGTAACCTGGGAGAGAGTTTGTATGAACAGCAGCTGATGCGAGAGAACTGAGG 277
QY 306 TCAGCTACACATACCTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAAATTGCAATTA 365
DB 278 TCAGTCTGTATGTTATGAAATCACAGAAAGCTTCTAGAAATGATAGGCTGTAT--CAAT 334
QY 366 ACAATGCTGTATCTTACTGCTGCCAGGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTT 425
DB 335 AACATTTTACTGTTTATAGGCAAGAACTTAATGAAAAAGTTATTTTAT-GAATTGAATTT 393
QY 426 TGATAAATAGTAAAGTCCAGGAGCTAAGAAATCAGACATCTTATGATGTTTCTAGATC 485
DB 394 TGTCAATTAGCAAAAGTATCACTTCAATCATGAAATTTGGCACTCTTTATTAGCTACTAG 453
QY 486 GAAAGACATAGTTGTATTGTGAACAAATCAGTATGATGGGTGGAGT 535
DB 454 GTTGAACCCCAAACTATTGTGAATAAAATCAATATGGTAAATGAACT 503

RESULT 12

US-09-704-424-17602
; Sequence 17602, Application US/09704424
; GENERAL INFORMATION:
; APPLICANT: Watson, James
; TITLE OF INVENTION: Polynucleotides, Polypeptides Expressed
; TITLE OF INVENTION: by the Polynucleotides and Methods for Their Use
; FILE REFERENCE: 11000.1045U
; CURRENT APPLICATION NUMBER: US/09/704,424
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 36881
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17602
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Mouse
US-09-704-424-17602

Query Match 13.7%; Score 175; DB 32; Length 323;
Best Local Similarity 94.8%; Pred. No. 1.8e-40;
Matches 181; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 130 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 189
DB 104 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCAGACTGTATCATTTAC 163
QY 190 GTGTGATGCGACATCATCAGCTCAAAACCGAGAGCAGCTGAGAGCGACTGTCTTC 249
DB 164 GTGTGATGCGACATCATCAGCTCAAAACCGAGAGCAGCTGAGAGCGACTGTCTTC 223

QY 250 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 309
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Db 224 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 283
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QY 310 CTACACATAC 320
|||||
Db 284 CTGACCTTCC 294
|||||

RESULT 13
US-09-704-424-16807
; Sequence 16807, Application US/09704424
; GENERAL INFORMATION:
; APPLICANT: Watson, James
; TITLE OF INVENTION: Polynucleotides, Polypeptides Expressed
; FILE REFERENCE: 11000.1045U
; CURRENT APPLICATION NUMBER: US/09/704,424
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 36881
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16807
; LENGTH: 340
; TYPE: DNA
; ORGANISM: Mouse
US-09-704-424-16807

Query Match 13.7%; Score 175; DB 32; Length 340;
Best Local Similarity 94.8%; Pred. No. 1.9e-40;
Matches 181; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 189
Db 117 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 176
|||||
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
Db 177 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 236
|||||
QY 250 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 309
Db 237 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 296
|||||
QY 310 CTACACATAC 320
Db 297 CTGACCTTCC 307
|||||

RESULT 14
US-09-704-424-21386
; Sequence 21386, Application US/09704424
; GENERAL INFORMATION:
; APPLICANT: Watson, James
; TITLE OF INVENTION: Polynucleotides, Polypeptides Expressed
; FILE REFERENCE: 11000.1045U
; CURRENT APPLICATION NUMBER: US/09/704,424
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 36881
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21386
; LENGTH: 370
; TYPE: DNA
; ORGANISM: Mouse
US-09-704-424-21386

Query Match 13.7%; Score 175; DB 32; Length 370;
Best Local Similarity 94.8%; Pred. No. 2e-40;
Matches 181; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 189
|||||

Db 112 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 171
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
Db 172 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 231
QY 250 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 309
Db 232 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 291
QY 310 CTACACATAC 320
Db 292 CTGACCTTCC 302
|||||

RESULT 15
US-09-704-424-18243
; Sequence 18243, Application US/09704424
; GENERAL INFORMATION:
; APPLICANT: Watson, James
; TITLE OF INVENTION: Polynucleotides, Polypeptides Expressed
; FILE REFERENCE: 11000.1045U
; CURRENT APPLICATION NUMBER: US/09/704,424
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 36881
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18243
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Mouse
US-09-704-424-18243

Query Match 13.7%; Score 175; DB 32; Length 400;
Best Local Similarity 94.8%; Pred. No. 2.1e-40;
Matches 181; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 189
Db 111 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 170
|||||
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
Db 171 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 230
QY 250 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 309
Db 231 TTGTAACCTGGGAGAGAACTTTGATGAAACGACAGCTGATGGCAGAAAAAAGTGGGTCTAC 290
QY 310 CTACACATAC 320
Db 291 CTGACCTTCC 301
|||||

Search completed: July 13, 2005, 00:45:09
Job time : 5885.03 secs

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 17:41:25 ; Search time 2543.5 Seconds
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Title: US-09-788-074-2

Perfect score: 1279
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16258531 seqs, 2355356875 residues

Total number of hits satisfying chosen parameters: 32517062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents NA New.*

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17: /cgn2_6/prodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	142.6	11.1	664	1	PCT-US05-11532-965 Sequence 965, App
2	142.6	11.1	664	2	PCT-US04-42360-985 Sequence 985, App
3	127.6	10.0	1378	13	US-11-136-527-3136 Sequence 3136, App
4	125	9.8	420	17	US-60-680-544-19719 Sequence 19719, A
5	125	9.8	420	17	US-60-680-473-19719 Sequence 19719, A
6	125	9.8	662	14	US-11-051-454-102 Sequence 102, App
7	125	9.8	662	17	US-60-651-235-2921 Sequence 2921, App
8	125	9.8	672	17	US-60-651-235-2918 Sequence 2918, App
9	125	9.8	1083	17	US-60-651-235-2920 Sequence 2920, App
10	125	9.8	45762	11	US-10-940-774A-16651 Sequence 16651, A
11	119.2	9.3	453	8	US-10-450-763-13607 Sequence 13607, A
12	118.6	9.3	1286	17	US-60-651-235-2919 Sequence 2919, App
13	118.6	9.3	13286	11	US-10-990-328A-97919 Sequence 97919, A
14	118.6	9.3	207317	11	US-10-990-328A-95342 Sequence 95342, A
15	102.2	8.0	1569	8	US-10-450-763-13606 Sequence 13606, A
16	102.2	8.0	1569	8	US-10-450-763-25344 Sequence 25344, A

17	94	7.3	598	8	US-10-450-763-27568 Sequence 27568, A
18	78.8	6.2	20183	13	US-11-066-316A-9920 Sequence 9920, App
19	78.8	6.2	80581	13	US-11-066-316A-9928 Sequence 9928, App
20	78.4	6.1	201	13	US-11-066-316A-26833 Sequence 26833, A
21	78.4	6.1	201	13	US-11-066-316A-26833 Sequence 26833, A
22	76.4	6.0	8524	11	US-10-940-774A-13282 Sequence 13282, A
23	73	5.7	201	11	US-10-990-328A-331909 Sequence 331909, A
24	73	5.7	201	11	US-10-990-328A-533079 Sequence 533079, A
25	71.2	5.6	925	17	US-60-680-544-19272 Sequence 19272, A
26	71.2	5.6	925	17	US-60-680-544-19731 Sequence 19731, A
27	71.2	5.6	925	17	US-60-680-473-19272 Sequence 19272, A
28	71.2	5.6	925	17	US-60-680-473-19731 Sequence 19731, A
29	70	5.5	620	11	US-10-940-774A-1540 Sequence 1540, App
30	70	5.5	636	13	US-11-090-997-1125 Sequence 1125, App
31	70	5.5	816	17	US-60-680-544-19390 Sequence 19390, A
32	70	5.5	816	17	US-60-680-473-19390 Sequence 19390, A
33	69.8	5.5	201	13	US-11-066-316A-3574 Sequence 3574, App
34	69.8	5.5	804	13	US-11-066-316A-205 Sequence 205, App
35	69.6	5.4	628	1	PCT-US05-00517-121 Sequence 121, App
36	69.4	5.4	399	17	US-60-680-544-47783 Sequence 47783, A
37	69.4	5.4	399	17	US-60-680-473-47783 Sequence 47783, A
38	67.4	5.3	201	13	US-11-066-316A-3569 Sequence 3569, App
39	67.4	5.3	1464	13	US-11-066-316A-204 Sequence 204, App
40	66.8	5.2	1153	17	US-60-680-544-19120 Sequence 19120, A
41	66.8	5.2	1153	17	US-60-680-473-19120 Sequence 19120, A
42	65.6	5.1	601	11	US-10-940-774A-42044 Sequence 42044, A
43	65.6	5.1	8597	11	US-10-940-774A-12945 Sequence 12945, A
44	65.4	5.1	753	13	US-11-136-527-1596 Sequence 1596, App
45	65.2	5.1	16596	17	US-60-659-397-12005 Sequence 12005, A

ALIGNMENTS

RESULT 1

PCT-US05-11532-965
; Sequence 965, Application PC/TUS0511532
; GENERAL INFORMATION:
; APPLICANT: Porter, Mark
; APPLICANT: Higgs, Brandon
; APPLICANT: Mendrick, Donna
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: HEPATOTOXICITY MOLECULAR MODELS
; FILE REFERENCE: 044921-5134-WO
; CURRENT APPLICATION NUMBER: PCT/US05/11532
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: US 60/559,949
; PRIOR FILING DATE: 2004-04-07
; NUMBER OF SEQ ID NOS: 2005
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 965
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US05-11532-965

Query Match	11.1%;	Score 142.6;	DB 1;	Length 664;
Best Local Similarity	84.7%;	Pred. No. 7.8e-30;		
Matches 160;	Conservative	0;	Mismatches 29;	Indels 0;
Gaps	0;			
QY	130	AGGAGTAGGAGCTCTTAGGAAGATGGCTGCCAAGCCAGACGTATCATTTAC	189	
Db	119	AGGAGTAGGAGCTCTTAGGAAGATGGCTGCCAAGCCAGACGTATCATTTAC	178	
QY	190	GTGTGATGTCACACATCAGGTCAAAACCCAGAGCAGTGAACACCACTGTGTCTC	249	
Db	179	CCTGACAAACAACTCACCCTCAAACTGAGAGCAGTGAACACCACTGTGTCTC	238	
QY	250	TTGTAACTCTGGGAGAGAGTTTGTGAAACGACAGCTGATGGCAGAAAACCTGAGGTAC	309	
Db	239	TTGACCTTGGGAGAGAGTTTGTGAAACGACAGCTGATGGCAGAAAACCTGAGGTAC	298	
QY	310	CTACAACAT	318	

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Db          299 CTGCACCTT 307
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Query Match      11.1%; Score 142.6; DB 2; Length 664;
Best Local Similarity 84.7%; Pred. No. 7.8e-30;
Matches 160; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db 119 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 178

Qy 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTTC 249
Db 179 CCTGCACACACACACTCACCGTCAAACTGAGAGACAGTGAAGACGACTGTGTCTTC 238

Qy 250 TTGTAACTGGGAGAGAAAGTTTGATGAAACGACAGCTGATGCGAGAAACACTGAGGTGAC 309
Db 239 TTGCACCTTGGGAGAGAAAGTTTGATGAAACGACAGCTGATGCGAGAAACACTGAGACGT 298

Qy 310 CTACAACAT 318
Db 299 CTGCACCTT 307

RESULT 3
US-11-136-527-3136
; Sequence 3136, Application US/11136527
; GENERAL INFORMATION:
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3136
; LENGTH: 1378
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (335)..(335)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (856)..(856)
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; OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-3136

Query Match      10.0%; Score 127.6; DB 13; Length 1378;
Best Local Similarity 62.4%; Pred. No. 1.8e-25;
Matches 118; Conservative 45; Mismatches 26; Indels 0; Gaps 0;

Qy 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db 315 WGGAGTGGGGYTGCCWCHWRNGAAGATGGWKCCATGSCCAACCCAGACTGCATCATTTWC 374

Qy 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTTC 249
Db 375 CCTGWCRCVCAMSARSSKACCGSDMDWBKSAGAGSACRGTGAAGACGACCGTCTTTTC 434

Qy 250 TTGTAACTGGGAGAGAAAGTTTGATGAAACGACAGCTGATGCGAGAAACACTGAGGTGAC 309
Db 435 TTSCACCTTGRGAGAGAGMWKKGATGAACCAACACAGCTGATGCGAGRRMACTGWRCCGT 494

Qy 310 CTACAACAT 318
Db 495 YTGCAWYTT 503

RESULT 4
US-60-680-544-19719
; Sequence 19719, Application US/60680544
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary
; FILE REFERENCE: 21590290000
; CURRENT APPLICATION NUMBER: US/60/680,544
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 19719
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Macaca Mulatta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(420)
; OTHER INFORMATION: n = A,T,C or G
US-60-680-544-19719

Query Match      9.8%; Score 125; DB 17; Length 420;
Best Local Similarity 78.8%; Pred. No. 6.5e-25;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db 142 AGGAGTGGGAATAGCTTTGCCAAAAATGGCGCAATGGCCAAAGCCAGACTGTATCATCAC 201

Qy 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGACAGTGAAGACGACTGTGTCTTC 249
Db 202 TTGTGATGGCAAAAACCTCACCATTAATAACTGAGAGACACTTTGAAAAACAACAGTTTC 261

Qy 250 TTGTAACTGGGAGAGAAAGTTTGATGAAACGACAGCTGATGCGAGAAACACTGAGGTGAC 309
Db 262 TTGTACCTCTGGGAGAGAAATTTGAAGAAACCAACAGCTGATGCGAGAAACACTCAGACTGT 321

Qy 310 CTACAACAT 318
Db 322 CTGCAGCTT 330
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RESULT 5
US-60-680-473-19719
; Sequence 19719, Application US/60680473
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary to
; FILE REFERENCE: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; CURRENT APPLICATION NUMBER: US/60/680,473
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 19719
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Macaca Mulatta
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(420)
; OTHER INFORMATION: n = A,T,C or G
US-60-680-473-19719

Query Match          9.8%; Score 125; DB 17; Length 420;
Best Local Similarity 78.8%; Pred. No. 6.5e-25;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 189
DB 142 AGGAGTGGGAATAGCTTTTGGGAATAATGGCCGAATGGCCAGCCAGACTGTATCATCAC 201
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 202 TTGTGATGGCAAAACCTCACCATATAAACTGAGAGCCTTTTGAAAAACAACAGTTTTC 261
QY 250 TTGTAACCTGGGAGAGAGTTTGTATGAACAGCAGCTGATGGCAGAAAACTGAGTCTAG 309
DB 262 TTGTACCTCTGGGAGAGAAATTTGAAGAAACCAACAGCTGATGGCAGAAAACTCAGACTGT 321
QY 310 CTACACAT 318
DB 322 CTGACGCTT 330

RESULT 6
US-11-051-454-102
; Sequence 102, Application US/11051454
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; FILE REFERENCE: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; CURRENT APPLICATION NUMBER: US/11/051,454
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/205,823

US-11-051-454-102
; Sequence 102, Application US/60680473
; GENERAL INFORMATION:
; APPLICANT: Cooper, Matthew
; APPLICANT: Kinch, Deborah
; APPLICANT: Rosenberg, Michael
; APPLICANT: Subramaniam, S. Sai
; APPLICANT: Szak, Suzanne
; APPLICANT: Li, Huo
; APPLICANT: Bandaru, Raj
; APPLICANT: Derbel, Maher
; TITLE OF INVENTION: Nucleotide Array Containing Polynucleotide Probes Complementary to
; FILE REFERENCE: Fragments of, Cynomolgus Monkey Genes and the Use Thereof
; CURRENT APPLICATION NUMBER: US/60/680,473
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 48714
; SOFTWARE: Patent Sequence Analysis Tool Version 1.0
; SEQ ID NO 19719
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Macaca Mulatta
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(420)
; OTHER INFORMATION: n = A,T,C or G
US-60-680-473-19719

Query Match          9.8%; Score 125; DB 17; Length 420;
Best Local Similarity 78.8%; Pred. No. 6.5e-25;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 189
DB 142 AGGAGTGGGAATAGCTTTTGGGAATAATGGCCGAATGGCCAGCCAGACTGTATCATCAC 201
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 202 TTGTGATGGCAAAACCTCACCATATAAACTGAGAGCCTTTTGAAAAACAACAGTTTTC 261
QY 250 TTGTAACCTGGGAGAGAGTTTGTATGAACAGCAGCTGATGGCAGAAAACTGAGTCTAG 309
DB 262 TTGTACCTCTGGGAGAGAAATTTGAAGAAACCAACAGCTGATGGCAGAAAACTCAGACTGT 321
QY 310 CTACACAT 318
DB 322 CTGACGCTT 330

RESULT 7
US-60-651-235-2921
; Sequence 2921, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2921
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-651-235-2921

Query Match          9.8%; Score 125; DB 17; Length 662;
Best Local Similarity 78.8%; Pred. No. 7.7e-25;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCCAAGCCAGACTGTATCATTTAC 189
DB 126 AGGAGTGGGAATAGCTTTTGGGAATAATGGCCGAATGGCCAGCCAGACTGTATCATCAC 185
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 186 TTGTGATGGTAATAAACCTCACCATATAAACTGAGAGCCTTTTGAAAAACAACAGTTTTC 245
QY 250 TTGTAACCTGGGAGAGAGTTTGTATGAACAGCAGCTGATGGCAGAAAACTGAGTCTAG 309
DB 246 TTGTACCTCTGGGAGAGAAATTTGAAGAAACCAACAGCTGATGGCAGAAAACTCAGACTGT 305
```

QY 310 CTACAACAT 318
|||
Db 306 CTGCAACTT 314

RESULT 8

US-60-651-235-2918
; Sequence 2918, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2918
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-651-235-2918

Query Match 9.8%; Score 125; DB 17; Length 672;
Best Local Similarity 78.8%; Pred. No. 7.7e-25;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTCAC 189
|||||
Db 136 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 195
|||||
QY 190 GTGTGATGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTC 249
|||||
Db 196 TTGTGATGTAATAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGATTTTC 255
|||||
QY 250 TTGTAACTGGGAGAGAAGTTTGTATGAACACGACACTGATGCGACAGAAAAAAGTGGGTGAG 309
|||||
Db 256 TTGTACCTGGGAGAGAAGTTTGAAGAAACCAACAGCTGATGCGACAGAAAAAAGTGGGTGAG 315
|||||
QY 310 CTACAACAT 318
|||
Db 316 CTGCAACTT 324

RESULT 9

US-60-651-235-2920
; Sequence 2920, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2920
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-651-235-2920

Query Match 9.8%; Score 125; DB 17; Length 1083;
Best Local Similarity 78.8%; Pred. No. 9.2e-25;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTCAC 189
|||||
Db 181 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 240
|||||
QY 190 GTGTGATGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTC 249
|||||
Db 241 TTGTGATGTAATAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGATTTTC 300
|||||
QY 250 TTGTAACTGGGAGAGAAGTTTGTGAACACGACAGCTGATGCGACAGAAAAAAGTGGGTGAG 309
|||||

Db 301 TTGTACCTGGGAGAGAAGTTTGAAGAAACCAACAGCTGATGCGAGAAAAAAGTGGGTGAG 360
|||||
QY 310 CTACAACAT 318
|||
Db 361 CTGCAACTT 369

RESULT 10

US-10-940-774A-16651/C
; Sequence 16651, Application US/10940774A
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/10/940,774A
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16651
; LENGTH: 45762
; TYPE: DNA
; ORGANISM: Human
US-10-940-774A-16651

Query Match 9.8%; Score 125; DB 11; Length 45762;
Best Local Similarity 78.8%; Pred. No. 3.5e-24;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTCAC 189
|||||
Db 28038 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 27979
|||||
QY 190 GTGTGATGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTC 249
|||||
Db 27978 TTGTGATGTAATAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACAGATTTTC 27919
|||||
QY 250 TTGTAACTGGGAGAGAAGTTTGTGAACACGACAGCTGATGCGAGAAAAAAGTGGGTGAG 309
|||||
Db 27918 TTGTACCTGGGAGAGAAGTTTGAAGAAACCAACAGCTGATGCGAGAAAAAAGTGGGTGAG 27859
|||||
QY 310 CTACAACAT 318
|||
Db 27858 CTGCAACTT 27850

RESULT 11

US-10-450-763-13607
; Sequence 13607, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 13607
; LENGTH: 453
; TYPE: DNA


```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (251)..(364)
; OTHER INFORMATION: 94% homologous to Bos taurus Lp2, accession number
; OTHER INFORMATION: U55188, Smith-Waterman Score=189.
US-10-450-763-13607

Query Match          9.3%; Score 119.2; DB 8; Length 453;
Best Local Similarity 58.4%; Pred. No. 3e-23;
Matches 250; Conservative 0; Mismatches 168; Indels 10; Gaps 2;

QY 400 AAAAATCTATTATGAGTGGCTTTTGTAAATTAATTAAGTCCAGACTTAACAAT 459
DB 11 AAAAAGTTTATGAAATTTGTTGCAAAATAGCAAAAGATATCAACTTCATCATAG 70
QY 460 GAAGACATCTTATGAGTCTTCTAGATCGAAAGCACATAGTTGTATTGTCAACAAAATCAG 519
DB 71 AATTGCGATCTTTTATTAGTACTAGTTGAAAACACCAAACTATTGTGATAAATCAA 130
QY 520 TATGATGGGTGGAGT-----TCAGAGAGGAAAGCGAAGACTTTGTGGAGT-----GG 569
DB 131 TATGGTAAATGAAGTAGACTCAGAAAGGAGAGGTGAAACAAATGTTGATTAAGGAGGT 190
QY 570 TGTGGTCTCTGGGGTCTTCTACTTTTGAAGATGATGAATCACTAACTACCTGTATTTTGG 629
DB 191 TATGAGTCTAGGAACTCTTGTAAATGCTTGAAGATTAAACCGTTTACTTTGTTTTTG 250
QY 630 CAGAGCGTCTGCACCTTCCAGAGCGTGCCTGTCAGCAGCAGCAGCAATGGGAGGAG 689
DB 251 CAGACTGTCTGCACTTTACAGATGGTGTGATTTGTTTCCAGATCAGAGTGGGATGGGAG 310
QY 690 GAGAGCAGCATAAACAGAAACTGAAGGATGGGAAGATGATCGTGTGAGCATCAAGCA 749
DB 311 GAAGCACAATAACAGAAATTTGAAGATGGGAATTAAGTGTGTGATGTCRAACTG 370
QY 750 CTGGCAACCATGCTGGAGTTGGGCTTCAGCAGCAGTTGTGATCAATCACTTCGGGTCAATG 809
DB 371 CTGTGCTCAGTCAGCTTCTTGTGTGCAATTCATAGTTTCATAACTGTTCTATATCATTTG 430
QY 810 GTTCTTTA 817
DB 431 ATCAITAA 438

RESULT 12
US-60-651-235-2919
; Sequence 2919, Application US/60651235
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001581
; CURRENT APPLICATION NUMBER: US/60/651,235
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 3512
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2919
; LENGTH: 1286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-651-235-2919

Query Match          9.3%; Score 118.6; DB 17; Length 1286;
Best Local Similarity 76.7%; Pred. No. 6.4e-23;
Matches 145; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 139 AGGAGTGGGAATAGCTTTTGCMAAAATATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 198
QY 190 GTGTGATGCAACAACATCACCGTCAAAACCCGAGACAGTGAAGACCACTGTGTCTTC 249
DB 199 TTGTGATGGCAGAACTCTCACCACAAAAAACCAGAGACACTTTTGAAGAAACACACAGTTTC 258
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QY 250 TTGTAACTCTGGGAGAGAGTTTGTATGAACAGACAGCTGATGGCAGAAAAAAGTGAAGTCAG 309
DB 259 TTGTACCTCTGGGAGAGCGAGTTTGAAGAAACACACAGCTGATGGCAGAAAAAAGTGAAGTCAG 318
QY 310 CTACAACAT 318
DB 319 CTGCAACTT 327

RESULT 13
US-10-990-328A-97919
; Sequence 97919, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97919
; LENGTH: 13286
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-990-328A-97919

Query Match          9.3%; Score 118.6; DB 11; Length 13286;
Best Local Similarity 76.7%; Pred. No. 1.5e-22;
Matches 145; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 6138 AGGAGTGGGAATAGCTTTGCMAAAATATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 6197
QY 190 GTGTGATGCAACAACATCACCGTCAAAACCCGAGACAGTGAAGACCACTGTGTCTTC 249
DB 6198 TTGTGATGCGAGAAACCTCACCACAAAAAACCAGAGACACTTTTGAAGAAACACACAGTTTC 6257
QY 250 TTGTAACTCTGGGAGAGAGTTTGTATGAACAGACAGCTGATGGCAGAAAAAAGTGAAGTCAG 309
DB 6258 TTGTACCTCTGGGAGAGAGTTTGAAGAAACCAACAGCTGATGGCAGAAAAAAGTGAAGTCAG 6317
QY 310 CTACAACAT 318
DB 6318 CTGCAACTT 6326

RESULT 14
US-10-990-328A-95342/c
; Sequence 95342, Application US/10990328A
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328A
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 55824
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95342
; LENGTH: 207317
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (207317)
; OTHER INFORMATION: n = A, T, C or G
US-10-990-328A-95342
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Query Match 9.3%; Score 118.6; DB 11; Length 207317;
Best Local Similarity 76.7%; Pred. No. 4e-22;
Matches 145; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
|||||
Db 51254 AGGAGTGGGAATAGCTTTTGCAGAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 51195
|||||
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGACAGATGAAGACGACTGTGTTCTC 249
|||||
Db 51194 TTTGTATGGCAGAAACCTCACCAAAAACCGAGAGCACTTTGAAAAACAACACAGTTTTTC 51135
|||||
QY 250 TTGTAACCTGGGAGAGAACTTTTGATGAACGACAGCTGATGGCAGAAAAAAGCTGAGGTGAG 309
|||||
Db 51134 TTGTACCTGGGAGAGAGGATTTTGAAGAAACCAACAGCTGATGGCAGAAAAACACAGACTGT 51075
|||||
QY 310 CTCAACAT 318
|||
Db 51074 CTGCAACT 51066
|||

RESULT 15
US-10-450-763-13606
; Sequence 13606, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 13606
; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (236)..(2971)
; OTHER INFORMATION: 100% homologous to Homo sapiens protein kinase C mu, accession
; OTHER INFORMATION: number X75756, Smith-Waterman Score=4804.
US-10-450-763-13606

Query Match 8.0%; Score 102.2; DB 8; Length 1569;
Best Local Similarity 78.7%; Pred. No. 3.1e-18;
Matches 122; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 164 ATGGCCAGCCAGACTGTATCATTTAGTGGCAACAACATCACGGTCAAAACCGAG 223
|||||
Db 1 ATGGCCAGCCAGATTGTATCATCTTGTATGCAAAAACCTCACCAATAAACTGAG 60
|||||
QY 224 AGCAGATGAAGACGACTGTGTTCTTTGTTAACTGGGAGAGAAAGTTGATGAAACGACA 283
|||||
Db 61 AGCACTTTGAAAACAACACAGTTTTCTGTGTACCTGGGAGAGAAAGTTTGAAGAAAAACA 120
|||||
QY 284 GCTGATGGCAGAAAACACTGAGTCACTACACAT 318
|||||
Db 121 GCTGATGGCAGAAAGAACTCAGACTGTTTGCACAT 155
|||||

Search completed: July 12, 2005, 22:16:13
Job time : 2545.5 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1279	100.0	1279	9	US-09-788-074-2		Sequence 2, Appli
2	176.6	13.8	933	21	US-10-764-420-1507		Sequence 1507, Ap
3	176.6	13.7	537	16	US-10-029-386-5224		Sequence 5224, Ap
4	165	12.9	1623	9	US-09-778-844-65		Sequence 65, Appl1
5	144.2	11.3	695	16	US-10-316-253-202		Sequence 202, App
6	144.2	11.3	704	16	US-10-316-253-198		Sequence 198, App
7	144.2	11.3	704	17	US-10-388-934-489		Sequence 489, App

QY 61 GGCCAGTGGGATGATAAGGAATGAATCCTTGGCTTATCATTTGTACAAATATACGTCATTTC

Db 61 GSCCAGTGGGATGATGAAGGAATGAATCCTTGCTTATCATTTGATCAAAATTACGTCAATTTTC 120
QY 121 CATACCCACAGAGTAGAGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTG 180
Db 121 CATACCCACAGAGTAGAGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTG 180
QY 181 TATCATTACGTGTGATGSCAACCAACATCACCGTCAAAACCCGAGAGCAGAGTGAAGACGAC 240
Db 181 TATCATTACGTGTGATGSCAACCAACATCACCGTCAAAACCCGAGAGCAGAGTGAAGACGAC 240
QY 241 TGTGTTCTCTTGTAACTCTGGGAGAGAAGTTTGAATGAACGACAGCTGATGGCAGAAAAAC 300
Db 241 TGTGTTCTCTTGTAACTCTGGGAGAGAAGTTTGAATGAACGACAGCTGATGGCAGAAAAAC 300
QY 301 TGAGTCACTGATCAACATACCTGTGAAGCGAAGAAGCTTCTAGATTTACAGATTAAGATTG 360
Db 301 TGAGTCACTGATCAACATACCTGTGAAGCGACAGAAAGCTTCTAGATTTACAGATTAAGATTG 360
QY 361 CATTAACAATGCTCTGACTTACTGCTCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTG 420
Db 361 CATTAACAATGCTCTGACTTACTGCTCAAGGGCTGACTGAAAAAACTACTTTATGGAGTTG 420
QY 421 ACTTTTGATAAATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCT 480
Db 421 ACTTTTGATAAATTAGTAAAGTCCAGGACTAAGAAATGAAGACATCTTATGAGTTTCT 480
QY 481 AGATCGAAAAAGCACATAGTTGATTTGTGAACAAAATCAGATGATGGGGTGGAGTTTCA 540
Db 481 AGATCGAAAAAGCACATAGTTGATTTGTGAACAAAATCAGATGATGGGGTGGAGTTTCA 540
QY 541 GAGGGAAGGCGAAGACTTGTGGAGTGTGTGGGTCTCTGGGGTCTCTTCACTTTGGAA 600
Db 541 GAGGGAAGGCGAAGACTTGTGGAGTGTGTGGGTCTCTGGGGTCTCTTCACTTTGGAA 600
QY 601 GATGATGAACCTAACCTACCTGATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGGCC 660
Db 601 GATGATGAACCTAACCTACCTGATTTTTCAGACGGTCTGCACCTTCCAAGACGGTGGCC 660
QY 661 TGGTCCAGCACAGCAATGGGACGGGAGGAGGACAGACAGTAAACAGAAAACTGAAGGATG 720
Db 661 TGGTCCAGCACAGCAATGGGACGGGAGGAGGACAGTAAACAGAAAACTGAAGGATG 720
QY 721 GGAAGATGATCTGTGTGAGCATCAAGCACTGCGACCATCTGCGATTTGGGCTCGACGCC 780
Db 721 GGAAGATGATCTGTGTGAGCATCAAGCACTGCGACCATCTGCGATTTGGGCTCGACGCC 780
QY 781 ACAGTTGTCAATACCACTTCGGGTCAATGGTTCTTTAAACAGAGAAGGAAACTTAGGAGG 840
Db 781 ACAGTTGTCAATACCACTTCGGGTCAATGGTTCTTTAAACAGAGAAGGAAACTTAGGAGG 840
QY 841 ACAATCTGAAAAATACAAAGTTAGAAAACGAGAGTCTCTATTCCTGAGGCGCCCTTTGG 900
Db 841 ACAATCTGAAAAATACAAAGTTAGAAAACGAGAGTCTCTATTCCTGAGGCGCCCTTTGG 900
QY 901 GGACGAGAGAGTGTGGGATCCAGATGTGGCTGAGAGAGCTGAGAGCTGGCAGGC 960
Db 901 GGACGAGAGAGTGTGGGATCCAGATGTGGCTGAGAGAGCTGAGAGCTGGCAGGC 960
QY 961 CACCGAGCAGCCCTCTCTGGTACATTTGAATCTGAGATGTGGTTTCTGTTAGGT 1020
Db 961 CACCGAGCAGCCCTCTCTGGTACATTTGAATCTGAGATGTGGTTTCTGTTAGGT 1020
QY 1021 AATAATTTAGATCATATCCAGTGTCTGAGTCTGAGGCGCAAAATATACATATAAC 1080
Db 1021 AATAATTTAGATCATATCCAGTGTCTGAGTCTGAGGCGCAAAATATACATATAAC 1080
QY 1081 AAAACAGAGCTCTAGTCTCTCTGATTTGAATCTGAGATGTGGTTTCTGTTAGGT 1140
Db 1081 AAAACAGAGCTCTAGTCTCTCTGATTTGAATCTGAGATGTGGTTTCTGTTAGGT 1140
QY 1141 TGGTTACAAGCGTTTATAGGATTTGCCCCAACACATGCTCTGAAATGTACAGTTGGCC 1200
Db 1141 TGGTTACAAGCGTTTATAGGATTTGCCCCAACACATGCTCTGAAATGTACAGTTGGCC 1200

QY 1201 TGAGACTCTATCTTTCTTCTCTAGGAGTGTGATGAACAATGCCACTGCACTCGGCT 1260
Db 1201 TGAGACTCTATCTTTCTTCTCTAGGAGTGTGATGAACAATGCCACTGCACTCGGCT 1260
QY 1261 CTATGAGAAGGTGCAATGA 1279
Db 1261 CTATGAGAAGGTGCAATGA 1279

RESULT 2

US-10-764-420-1507
; Sequence 1507, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
; APPLICANT: Lum, Pek Yee
; APPLICANT: Tan, Yejun
; APPLICANT: Dai, Hongyue
; TITLE OF INVENTION: Methods For Determining Whether An Agent Possesses A Defined Biological Activity
; FILE REFERENCE: ROSA122057
; CURRENT APPLICATION NUMBER: US/10/764,420
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US 60/442,797
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: US 60/474,413
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1507
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-764-420-1507

Query Match 13.8%; Score 176.6; DB 21; Length 933;
Best Local Similarity 95.3%; Pred. No. 4.2e-42;
Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 130 AGGAGTAGAGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
Db 112 AGGAGTAGAGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 171
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 249
Db 172 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 231
QY 250 TTGTAACCTGGGAGAGAAAGTTTGATGAAAACGACAGCTGATGGCAGAAAACTGAGGTGAG 309
Db 232 TTGTAACCTGGGAGAGAAAGTTTGATGAAAACGACAGCTGATGGCAGAAAACTGAGACGCT 291
QY 310 CTACAAACATAC 320
Db 292 CTGCACCTTCC 302

RESULT 3

US-10-029-386-5224
; Sequence 5224, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 5224
; LENGTH: 537

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF181449.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EST HUMAN HIT: AA428498.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q01469, EVALUE 1.00e-27
; OTHER INFORMATION: NT HIT: g113642859, EVALUE 2.00e-93
US-10-029-386-5224

Query Match      13.7%; Score 175.6; DB 16; Length 537;
Best Local Similarity 67.6%; Pred. No. 6.1e-42;
Matches 277; Conservative 0; Mismatches 129; Indels 4; Gaps 2;

QY 126 CCACGAGGTAGGACTGGCTCTTAGGAAGATGCTGCCATGGCCAAAGCCAGACGAGTGTATCA 185
DB 98 CTACAGGAGTGGGAATAGCTTTCCGAAANAATGGCGCAATGGCCAAAGCCAGATGTATCA 157
QY 186 TTACGTGTGATGCAACAACATCACCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGT 245
DB 158 TCACCTGTGTGATAAACCCTCACCATAAACTGAGAGCACTTTGNAACAACACACT 217
QY 246 TCTCTGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAGAAAAAAGTGGG 305
DB 218 TTTCTTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAGAAAAAAGTGGG 277
QY 306 TCAGCTACACATCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAAATTCATTA 365
DB 278 TCAGTCGTGACATGTTATGAATATCAGAGAGCTTCTAGAAATGATAGGCTGTAT---CAAT 334
QY 366 ACAATCTCTGTACTTACTGCGAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTT 425
DB 335 AACATTTTACTGTTTATAGCGAAGACTTAATGAAAAAGTTATTTAT-GAATTGAATTT 393
QY 426 TGATAAATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTAAGAGTTTCTAGATC 485
DB 394 TGTCAAATTAGCAAAAGTATCAACTTCATCATAGAAATGGCATCTTTTATAGCTACTAG 453
QY 486 GAAAGCACATAGTCTTATGTCACAAATATCATGATGGGTGAGCT 535
DB 454 GTTGAACACCAAACTATTGTGAATAAATCAATATGGTTAATGAAGT 503

RESULT 4
US-09-778-844-65
; Sequence 65, Application US/09778844
; Patent No. US20020150971A1
; GENERAL INFORMATION:
; APPLICANT: JOHANSEN, JEANETTE ELISABETH
; APPLICANT: SCHALLING, MARTIN
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES FOR CONTROLLING FOOD
; TITLE OF INVENTION: INTAKE AND/OR BODY WEIGHT
; FILE REFERENCE: 030307/0195
; CURRENT APPLICATION NUMBER: US/09/778,844
; CURRENT FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Mus Musculus
US-09-778-844-65

Query Match      12.9%; Score 165; DB 9; Length 1623;
Best Local Similarity 92.1%; Pred. No. 1.8e-38;
Matches 174; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 612 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 671

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AF181449.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.5
; OTHER INFORMATION: EST HUMAN HIT: AA428498.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q01469, EVALUE 1.00e-27
; OTHER INFORMATION: NT HIT: g113642859, EVALUE 2.00e-93
US-10-029-386-5224

Query Match      13.7%; Score 175.6; DB 16; Length 537;
Best Local Similarity 67.6%; Pred. No. 6.1e-42;
Matches 277; Conservative 0; Mismatches 129; Indels 4; Gaps 2;

QY 126 CCACGAGGTAGGACTGGCTCTTAGGAAGATGCTGCCATGGCCAAAGCCAGACGAGTGTATCA 185
DB 98 CTACAGGAGTGGGAATAGCTTTCCGAAANAATGGCGCAATGGCCAAAGCCAGATGTATCA 157
QY 186 TTACGTGTGATGCAACAACATCACCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGT 245
DB 158 TCACCTGTGTGATAAACCCTCACCATAAACTGAGAGCACTTTGNAACAACACACT 217
QY 246 TCTCTGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAGAAAAAAGTGGG 305
DB 218 TTTCTTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAGAAAAAAGTGGG 277
QY 306 TCAGCTACACATCTGTGAAGCGACAGAGCTTCTAGATTTACAGATTAAATTCATTA 365
DB 278 TCAGTCGTGACATGTTATGAATATCAGAGAGCTTCTAGAAATGATAGGCTGTAT---CAAT 334
QY 366 ACAATCTCTGTACTTACTGCGAAGGCTGACTGAAAAAACTACTTTATGGAGTTGACTTT 425
DB 335 AACATTTTACTGTTTATAGCGAAGACTTAATGAAAAAGTTATTTAT-GAATTGAATTT 393
QY 426 TGATAAATTAGTAAAGTCCCGAGGACTAAGAAATGAAGACATCTTAAGAGTTTCTAGATC 485
DB 394 TGTCAAATTAGCAAAAGTATCAACTTCATCATAGAAATGGCATCTTTTATAGCTACTAG 453
QY 486 GAAAGCACATAGTCTTATGTCACAAATATCATGATGGGTGAGCT 535
DB 454 GTTGAACACCAAACTATTGTGAATAAATCAATATGGTTAATGAAGT 503

RESULT 5
US-10-316-253-202
; Sequence 202, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Peng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 695
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (59)..(466)
; OTHER INFORMATION:
US-10-316-253-202

Query Match      11.3%; Score 144.2; DB 16; Length 695;
Best Local Similarity 85.2%; Pred. No. 2.2e-32;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 136 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 195
QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTCTC 249
DB 196 CCTGACGCGCAACACCTCACCGTCAAAACTGAGAGCAGCGTGAAGACCGCTGTTTC 255
QY 250 TTGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCAGAAAAAAGTGGG 309
DB 256 TTGCACCTTTGGGAGAGAGTTTGTATGAACCAACCAAGCTGATGGCAGAAAAAAGTGGG 315
QY 310 CTACAACAT 318
DB 316 CTGCACCTT 800

RESULT 6
US-10-316-253-198
; Sequence 198, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Peng
; APPLICANT: Greis, Kenneth
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; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 198
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)..(451)
; OTHER INFORMATION:
US-10-316-253-198

Query Match      11.3%; Score 144.2; DB 16; Length 704;
Best Local Similarity 85.2%; Pred. No. 2.2e-32;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 121 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 180
QY 190 GTGTATGGCAACAACATCAGCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 181 CCTGACGGCAACAACCTCACCGTCAAAACCTGAGAGCAGCGTGAAGACGACCGTGTTC 240
QY 250 TTGTAACCTGGGAGAGAGTTTGTGTAAGACGACACTGTATGCAAGAAACCTGAGGTCA 309
DB 241 TTGCACCTTGGGAGAGAGTTTGTGTAAGAAACCAACAGCTGTATGCGAGAAACCTGAGAC 300

QY 310 CTACAACAT 318
DB 301 CTGCACCTT 309

RESULT 7
US-10-388-934-489
; Sequence 489, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boese, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 489
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-388-934-489

Query Match      11.3%; Score 144.2; DB 17; Length 704;
Best Local Similarity 85.2%; Pred. No. 2.2e-32;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 121 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 180
QY 190 GTGTATGGCAACAACATCAGCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249

QY 250 TTGTAACCTGGGAGAGAGTTTGTGTAAGACGACACTGTATGCAAGAAACCTGAGGTCA 309
DB 241 TTGCACCTTGGGAGAGAGTTTGTGTAAGAAACCAACAGCTGTATGCGAGAAACCTGAGAC 300

QY 310 CTACAACAT 318
DB 301 CTGCACCTT 309

RESULT 8
US-10-191-803-522
; Sequence 522, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 522
; LENGTH: 704
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 S69874
US-10-191-803-522

Query Match      11.3%; Score 144.2; DB 17; Length 704;
Best Local Similarity 85.2%; Pred. No. 2.2e-32;
Matches 161; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
DB 121 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 180
QY 190 GTGTATGGCAACAACATCAGCGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
DB 181 CCTGACGGCAACAACCTCACCGTCAAAACCTGAGAGCAGCGTGAAGACGACCGTGTTC 240
QY 250 TTGTAACCTGGGAGAGAGTTTGTGTAAGACGACACTGTATGCAAGAAACCTGAGGTCA 309
DB 241 TTGCACCTTGGGAGAGAGTTTGTGTAAGAAACCAACAGCTGTATGCGAGAAACCTGAGAC 300

QY 310 CTACAACAT 318
DB 301 CTGCACCTT 309

RESULT 9
US-10-316-253-200
; Sequence 200, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
```

; APPLICANT: Wang, Feng
 ; APPLICANT: Greis, Kenneth
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins
 ; FILE REFERENCE: 8865M
 ; CURRENT APPLICATION NUMBER: US/10/316,253
 ; CURRENT FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: US 60/355,295
 ; PRIOR FILING DATE: 2002-02-08
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 200
 ; LENGTH: 664
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (42)..(449)
 ; OTHER INFORMATION:
 ; US-10-316-253-200
 ;
 Query Match 11.1%; Score 142.6; DB 16; Length 664;
 Best Local Similarity 84.7%; Pred. No. 6.5e-32;
 Matches 160; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
 DB 119 AGGAGTAGGCTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 178
 QY 190 GTGTGATGGCAACAACATCACCGTCAAAACCCGAGACAGTGAAGACGACGTGTTCTC 249
 DB 179 CTTGCAACAACACCTCACCGTCAAAACCTGAGAGACAGTGAAGACGACGTGTTCTC 238
 QY 250 TTGTAACCTGGGAGAGAGATTTGATGAACACGACAGCTGATGGCAGAAAACTGAGGTCAG 309
 DB 239 TTGCACCTTTGGGAGAGAGATTTGATGAACACGACAGCTGATGGCAGAAAACTGAGGTCAG 298
 QY 310 CTACAACAT 318
 DB 299 CTGCACCTT 307
 ;
 RESULT 10
 US-10-333-872A-4/c
 ; Sequence 4, Application US/10333872A
 ; Publication No. US20040265804A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Forschungszentrum Karlsruhe GmbH
 ; TITLE OF INVENTION: Method for identifying metastatic tumor cells
 ; FILE REFERENCE: US 10/333,872
 ; CURRENT APPLICATION NUMBER: US/10/333,872A
 ; CURRENT FILING DATE: 2003-01-24
 ; NUMBER OF SEQ ID NOS: 289
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 335
 ; TYPE: DNA
 ; ORGANISM: rat
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(335)
 ; OTHER INFORMATION: Clone #6 (MLSSH)
 ; US-10-333-872A-4
 ;
 Query Match 10.1%; Score 129.8; DB 20; Length 335;
 Best Local Similarity 82.2%; Pred. No. 3.2e-28;
 Matches 157; Conservative 3; Mismatches 30; Indels 1; Gaps 1;
 QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCC-ATGGCCAAAGCCAGACTGTATCATTTA 188
 DB 305 AGGAGTAGGCTGGCTCTTAGGAGAGTGGTGMATGGCCAAACGACAGCTGCATCATTA 246
 QY 189 CGTGTGATGGCAACAACATCACCGTCAAAACCCGAGACAGTGAAGACGACTGTGTTCT 248

;
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43253
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-43253

Query Match 9.8%; Score 125; DB 18; Length 333;
Best Local Similarity 78.8%; Pred. No. 9e-27;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 189
Db |||||
73 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 132
QY 190 GTGTGATGGCAACATCACGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 249
Db |||||
133 TTGTGATGGTAAAAAACCCTCACATAAAACTGAGAGCACTTTGAAAAACAACACAGTTTTC 192
QY 250 TTGTAACTGGGAGAGAGTTTGTATGAAACGACAGCTGATGGCAGAAAAAAGCTGAGGTCAG 309
Db |||||
193 TTGTACCTGGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAGAAAAAAGCTGAGGTCAG 252
QY 310 CTACAACAT 318
Db |||||
253 CTGCAACTT 261

RESULT 13
US-09-804-014A-46
; Sequence 46, Application US/09804014A
; Publication No. US20030064489A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Vernet, Corine
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinketsu, Richard
; APPLICANT: Spaderna, Steven
; APPLICANT: Majumder, Kumud
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-721 US
; CURRENT APPLICATION NUMBER: US/09/804,014A
; PRIOR FILING DATE: 2002-04-24
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/188,316
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/188,277
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/189,139
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/189,140
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: 60/190,401
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/190,231
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-804-014A-46

Query Match 9.8%; Score 125; DB 10; Length 406;
Best Local Similarity 78.8%; Pred. No. 1e-26;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 189

Db |||||
76 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 135
QY 190 GTGTGATGGCAACATCACGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 249
Db |||||
136 TTGTGATGGTAAAAAACCCTCACATAAAACTGAGAGCACTTTGAAAAACAACACAGTTTTC 195
QY 250 TTGTAACTGGGAGAGAGTTTGTATGAAACGACAGCTGATGGCAGAAAAAAGCTGAGGTCAG 309
Db |||||
196 TTGTACCTGGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAGAAAAAAGCTGAGGTCAG 255
QY 310 CTACAACAT 318
Db |||||
256 CTGCAACTT 264

RESULT 14
US-10-242-535A-7126
; Sequence 7126, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7126
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-7126

Query Match 9.8%; Score 125; DB 17; Length 439;
Best Local Similarity 78.8%; Pred. No. 1.1e-26;
Matches 149; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAAGCCAGCAGCTGTATCATTTAC 189
Db |||||
123 AGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATCATCAC 182
QY 190 GTGTGATGGCAACATCACGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTTCTC 249
Db |||||
183 TTGTGATGGTAAAAAACCCTCACATAAAACTGAGAGCACTTTGAAAAACAACACAGTTTTC 242
QY 250 TTGTAACTGGGAGAGAGTTTGTATGAAACGACAGCTGATGGCAGAAAAAAGCTGAGGTCAG 309
Db |||||
243 TTGTACCTGGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAGAAAAAAGCTGAGGTCAG 302
QY 310 CTACAACAT 318
Db |||||
303 CTGCAACTT 311

RESULT 15
US-10-085-783A-7126
; Sequence 7126, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002

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OM nucleic - nucleic search, using sw model

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(without alignments)
9372.119 Million cell updates/sec

Title: US-09-788-074-4
Perfect score: 662
Sequence: 1 accgcgcagcagaccctc.....taataaatgtgttgcgt 662

Scoring table: IDENTITY_NUC
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Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: geneseqn2001bs.*
6: geneseqn2002as.*
7: geneseqn2002bs.*
8: geneseqn2003as.*
9: geneseqn2003bs.*
10: geneseqn2003cs.*
11: geneseqn2003ds.*
12: geneseqn2004as.*
13: geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	662	100.0	662	AAS13247	Aas13247 Human DNA
2	662	100.0	662	ABV77978	ABV77978 Hypoxia-r
3	662	100.0	662	ADB75278	ADB75278 Prostate
4	662	100.0	662	ADH28827	ADH28827 Human chr
5	662	100.0	662	ADJ75120	ADJ75120 Marker ge
6	662	100.0	662	ADN03852	ADN03852 Antipsori
7	662	100.0	662	ADO19263	ADO19263 Human PRO
8	662	100.0	662	ADP13321	ADP13321 Renal cel
9	662	100.0	662	ADR24747	ADR24747 Breast ca
10	662	100.0	662	ACN38822	ACN38822 Tumour-as
11	662	100.0	662	ADP54337	ADP54337 Human PRO
12	662	100.0	662	ADR52981	ADR52981 Drug ther
13	662	100.0	662	ADP25373	ADP25373 PRO polyp
14	662	100.0	662	ADR99018	ADR99018 Fatty aci
15	662	100.0	662	ADR66234	ADR66234 Human pro
16	662	100.0	662	ADR66576	ADR66576 Human pro
17	660	99.7	720	AAZ77538	AAZ77538 Human ova
18	660	99.7	1071	ADB47413	ADB47413 Human cdn
19	660	99.7	1071	ADM86791	ADM86791 Human cdn
20	649	98.0	1072	AAS94888	Aas94888 Human DNA

21	625.6	94.5	681	13	ACN39645	Acn39645 Tumour-as
22	618.4	93.4	660	12	ADQ86530	Adq86530 Human tum
23	616.8	93.2	644	13	ACN39640	Acn39640 Tumour-as
24	590	89.1	615	6	ABK53828	Abk53828 Human hea
25	588	88.8	698	5	AA991764	Aa991764 DNA encod
26	583	88.1	606	6	ABK53952	Abk53952 Human hea
27	543.2	82.1	627	9	AAU57420	Aad57420 Human fat
28	535.6	80.9	634	6	ABS59331	Ab59331 Human fat
29	535.6	80.9	634	10	ADJ38435	Adj38435 Human cdn
30	533.2	80.5	612	10	ADK11762	Adk11762 Breast ca
31	517	78.1	555	6	ABK53861	Abk53861 Human hea
32	512	77.3	519	6	ABK53994	Abk53994 Human hea
33	500	75.5	566	6	ABK53874	Abk53874 Human hea
34	481.4	72.7	540	9	AAU57419	Aad57419 Human fat
35	476.4	72.0	494	9	ACH35892	Ach35892 Human end
36	474.2	71.6	588	9	ACH27751	Ach27751 Human adu
37	460.8	69.6	491	6	ABK92039	Abk92039 DNA encod
38	451	68.1	461	6	ABK53980	Abk53980 Human hea
39	439.4	66.4	501	12	ACH70818	Ach70818 Human gen
40	429.8	64.9	479	9	ACH38376	Ach38376 Human end
41	408	61.6	408	2	AAQ66842	Aaq66842 Melanogen
42	406	61.3	435	8	ACD13195	Ac13195 cDNA enco
43	395.8	59.8	410	10	ADK11763	Adk11763 Breast ca
44	367	55.4	413	5	AAS13344	Aas13344 Human cdn
45	365.6	55.2	499	5	AAS13343	Aas13343 Human cdn

ALIGNMENTS

RESULT 1
AAS13247
ID AAS13247 standard; DNA; 662 BP.
XX
AC AAS13247;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding keratinocyte fatty acid binding protein, Mall.
XX
KW Human; Mall 1; keratinocyte fatty acid binding protein; ds; anorectic;
KW antidiabetic; antilipemic; antiatherosclerotic; obesity; diabetes;
KW dyslipidaemia; atherosclerosis; antisense therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 49..456
FT /tag= a
FT /product= "Mall 1"
FT polyA_signal 645..650
FT /tag= b
XX
XX WO200160384-A1.
PN 23-AUG-2001.
PD 16-FEB-2001; 2001WO-US005019.
PP 17-FEB-2000; 2000US-0183106P.
PR (HARD) HARVARD COLLEGE.
XX
XX Hotamisligil GS;
XX WPI; 2001-570550/64.
XX P-PSDB; AAU08674.
XX Reducing the level of circulating free fatty acids in a mammal, useful
XX for treating or preventing obesity, diabetes, dyslipidemia or
XX atherosclerosis, by administering a keratinocyte lipid binding protein
XX inhibitor.

QY 181 ATCACTGTGATGGTAAACCTCACCATAAATACTGAGGCACTTTGAAACACACAG 240
 Db |||||
 QY 181 ATCACTGTGATGGTAAACCTCACCATAAATACTGAGGCACTTTGAAACACACAG 240
 Db |||||
 QY 241 TTTTCTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAAAAACCTCAG 300
 Db |||||
 QY 241 TTTTCTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAAAAACCTCAG 300
 Db |||||
 QY 301 ACTGCTGCAACTTTACAGATGTGCAATGGTTTCAGCATCAGAGTGGGATGGGAAGAA 360
 Db |||||
 QY 301 ACTGCTGCAACTTTACAGATGTGCAATGGTTTCAGCATCAGAGTGGGATGGGAAGAA 360
 Db |||||
 QY 361 AGCACAATAACAGAAATTTGAAGATGGGAATTTAGTGGAGTGTCTCATGACAAAT 420
 Db |||||
 QY 361 AGCACAATAACAGAAATTTGAAGATGGGAATTTAGTGGAGTGTCTCATGACAAAT 420
 Db |||||
 QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAAAATTCATCATCACTTTGGACAG 480
 Db |||||
 QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAAAATTCATCATCACTTTGGACAG 480
 Db |||||
 QY 481 GAGTTAATTAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTGTTTCTTT 540
 Db |||||
 QY 481 GAGTTAATTAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTGTTTCTTT 540
 Db |||||
 QY 541 CTTTCTTTTTCATTTACTGTTTCAATTTATCTTTATCAATAAATTTTACATGCGACTAT 600
 Db |||||
 QY 541 CTTTCTTTTTCATTTACTGTTTCAATTTATCTTTATCAATAAATTTTACATGCGACTAT 600
 Db |||||
 QY 601 TTTCAAGTGTGTTGGATTAAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
 Db |||||
 QY 601 TTTCAAGTGTGTTGGATTAAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
 Db |||||
 QY 661 CT 662
 Db ||
 QY 661 CT 662
 Db ||

RESULT 3

ADB75278
 ID ADB75278 standard; cdna; 662 BP.
 XX
 AC ADB75278;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Prostate cancer marker cDNA.
 XX
 KW Prostate; cancer; cytostatic; gene therapy; marker; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003009814-A2.
 XX
 PD 06-FEB-2003.
 XX
 PF 25-JUL-2002; 2002WO-US023913.
 XX
 PR 25-JUL-2001; 2001US-0307982P.
 PR 22-AUG-2001; 2001US-0314356P.
 PR 25-SEP-2001; 2001US-0325020P.
 PR 12-DEC-2001; 2001US-0341746P.
 PR 05-MAR-2002; 2002US-0362158P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
 PI Hoersht S, Kamatkar S, Wonsley AM, Glatt K, Zhao X, Anderson D;
 XX
 DR WPI; 2003-248033/24.
 XX
 PT New nucleic acid molecule, useful for diagnosing or treating prostate
 PT cancer.
 XX

PS Disclosure; SEQ ID NO 102; 99pp; English.
 XX
 CC The invention relates to newly discovered cancer markers associated with
 CC the cancerous state of prostate cells. Also disclosed is a method of
 CC assessing whether a patient is afflicted with prostate cancer. The method
 CC of the invention involves assessing whether a patient is afflicted with
 CC prostate cancer by comparing the level of expression of a marker in a
 CC patient sample and the normal level of expression of the marker in a
 CC control non-prostate cancer sample, where a significant increase in the
 CC level of expression of the marker in the patient sample and the normal
 CC level indicates that the patient is afflicted with prostate cancer.
 CC Nucleic acids of the invention are useful for diagnosing or treating
 CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;
 Query Match 100.0%; Score 662; DB 10; Length 662;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-164;
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGCGGAGCGAGACCCCTCTCTGACGCGCAGCCGCCGCCGCCACCCACCCAGATT 60
 Db |||||
 QY 1 ACCGCGGAGCGAGACCCCTCTCTGACGCGCAGCCGCCGCCGCCACCCACCCAGATT 60
 Db |||||
 QY 61 CAGCAGCTGGAAGGAGATGGCGCTTGGGAGCAGCAAGGCTTTGATGAATACATGAAG 120
 Db |||||
 QY 61 CAGCAGCTGGAAGGAGATGGCGCTTGGGAGCAGCAAGGCTTTGATGAATACATGAAG 120
 Db |||||
 QY 121 GAGCTAGGAGTGGGAATAGCTTTGGCAAAAATGGGCGCAATGGCCAGCAGATTGTATC 180
 Db |||||
 QY 121 GAGCTAGGAGTGGGAATAGCTTTGGCAAAAATGGGCGCAATGGCCAGCAGATTGTATC 180
 Db |||||
 QY 181 ATCACTGTGATGTTAAACCTCACCATAAATACTGAGAGCAGCTTTGAAAACACACAG 240
 Db |||||
 QY 181 ATCACTGTGATGTTAAACCTCACCATAAATACTGAGAGCAGCTTTGAAAACACACAG 240
 Db |||||
 QY 241 TTTTCTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAAAAACCTCAG 300
 Db |||||
 QY 241 TTTTCTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGATGGCAAAAACCTCAG 300
 Db |||||
 QY 301 ACTGCTGCAACTTTACAGATGTGCAATGGTTTCAGCATCAGAGTGGGATGGGAAGAA 360
 Db |||||
 QY 301 ACTGCTGCAACTTTACAGATGTGCAATGGTTTCAGCATCAGAGTGGGATGGGAAGAA 360
 Db |||||
 QY 361 AGCACAATAACAGAAATTTGAAGATGGGAATTTAGTGGAGTGTCTCATGACAAAT 420
 Db |||||
 QY 361 AGCACAATAACAGAAATTTGAAGATGGGAATTTAGTGGAGTGTCTCATGACAAAT 420
 Db |||||
 QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAAAATTCATCATCACTTTGGACAG 480
 Db |||||
 QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAAAATTCATCATCACTTTGGACAG 480
 Db |||||
 QY 481 GAGTTAATTAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTGTTTCTTT 540
 Db |||||
 QY 481 GAGTTAATTAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTGTTTCTTT 540
 Db |||||
 QY 541 CTTTCTTTTTCATTTACTGTTTCAATTTATCTTTATCAATAAATTTTACATGCGACTAT 600
 Db |||||
 QY 541 CTTTCTTTTTCATTTACTGTTTCAATTTATCTTTATCAATAAATTTTACATGCGACTAT 600
 Db |||||
 QY 601 TTTCAAGTGTGTTGGATTAAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
 Db |||||
 QY 601 TTTCAAGTGTGTTGGATTAAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
 Db |||||
 QY 661 CT 662
 Db ||
 QY 661 CT 662
 Db ||

```
RESULT 4
ADH28827 standard; DNA; 662 BP.
XX
AC
XX
DT 11-MAR-2004 (first entry)
XX
DE Human chronic myelogenous leukaemia (CML) gene marker #95.
XX
KW ds; chronic phase chronic myelogenous leukaemia; CP-CML;
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;
KW gene marker.
XX
OS Homo sapiens.
XX
PN US2003104426-A1.
XX
PD 05-JUN-2003.
XX
PF 14-JUN-2002; 2002US-00171581.
XX
PR 18-JUN-2001; 2001US-0298914P.
XX
PA (LINS//) LINSLEY P S.
PA (MAOM//) MAO M.
PA (DAIH//) DAI H.
PA (HEY//) HE Y.
PA (RADI//) RADICH J P.
XX
PI Linsley PS, Mao M, Dai H, He Y, Radich JP;
XX
DR WPI; 2003-787046/74.
XX
PT Classifying cell sample as chronic phase chronic myelogenous leukemia or
PT blast crisis chronic myelogenous leukemia by detecting difference in
PT expression of genes corresponding to the markers such as X15415, U89436.
XX
PS Disclosure; SEQ ID NO 95; 31pp; English.
XX
CC The invention relates to a method of classifying a cell sample as chronic
CC phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-
CC CML). The method is useful for classifying a sample as CP-CML or BC-CML.
CC The present sequence represents a human chronic myelogenous leukaemia
CC (CML) gene marker used to distinguish blast crisis CML from chronic phase
CC CML.
XX
SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 10; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.3e-164;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGCGGACGACAGCCCTCTCTGACGCGCAGCCGCGCCGACCCACCATGGCCACAGTT 60
DB 1 ACCGCGGACGACAGCCCTCTCTGACGCGCAGCCGCGCCGACCCACCATGGCCACAGTT 60
QY 61 CAGCAGCTGGAAGGAAGATGGCGCTGTGGGACAGCAAAAGGCTTGTGATGAATACATGAAG 120
DB 61 CAGCAGCTGGAAGGAAGATGGCGCTGTGGGACAGCAAAAGGCTTGTGATGAATACATGAAG 120
QY 121 GAGCTAGGAGTGGGAATAGCTTTGGGAAAATGGGCAATGGCCAAAGGCTTGTGATGATC 180
DB 121 GAGCTAGGAGTGGGAATAGCTTTGGGAAAATGGGCAATGGCCAAAGGCTTGTGATGATC 180
QY 181 ATCACTTGTGATGTTAAACCTCCACATAAAACCTGAGAGCACTTTGAAAAACAACACAG 240
DB 181 ATCACTTGTGATGTTAAACCTCCACATAAAACCTGAGAGCACTTTGAAAAACAACACAG 240
QY 241 TTTTCTTGACCTGGGAGAGAGTTTGAAGAAACACAGCTGATGGGCAAAAACTGAG 300
DB 241 TTTTCTTGACCTGGGAGAGAGTTTGAAGAAACACAGCTGATGGGCAAAAACTGAG 300

301 ACTGCTGCACAACTTTTACAGATGGTGCATTGGTTGAGCATCAGGAGTGGGATGGGAAGAA 360
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301 ACTGCTGCACAACTTTTACAGATGGTGCATTGGTTGAGCATCAGGAGTGGGATGGGAAGAA 360
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AGCACAATAACAAGAAATTTGAAAGATGGGAAAATTTAGTGGTGGAGTGTGTATGAACAAT 420
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 AGCACAATAACAAGAAATTTGAAAGATGGGAAAATTTAGTGGTGGAGTGTGTATGAACAAT 420
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 GTCACCTGTACTCGGATCTATGAAAAGTGAATAAATAATTCATCATCTTTGGACAG 480
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
421 GTCACCTGTACTCGGATCTATGAAAAGTGAATAAATAATTCATCATCTTTGGACAG 480
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GAGTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTCTTTT 540
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
481 GAGTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTCTTTT 540
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 CTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATATAAACATTTTACATGACGCTAT 600
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
541 CTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATATAAACATTTTACATGACGCTAT 600
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 TTCAAAGTGTGTGGATTAAATAGGATCATCCCTTTGGTTAATAATAAATGTTTGTG 660
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
601 TTCAAAGTGTGTGGATTAAATAGGATCATCCCTTTGGTTAATAATAAATGTTTGTG 660
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 CT 662
DB ||
661 CT 662

RESULT 5
ADJ75120
ID ADJ75120 standard; DNA; 662 BP.
XX
AC ADJ75120;
XX
DT 20-MAY-2004 (first entry)
XX
DE Marker gene SEQ ID NO:372.
XX
KW bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker gene; gene; ds.
XX
OS Homo sapiens.
XX
PN EPI394274-A2.
XX
PD 03-MAR-2004.
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
PR 06-AUG-2002; 2002JP-00229312.
PR 20-MAR-2003; 2003JP-00077212.
XX
PA (GENO-) GENOX RES INC.
XX
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX
DR WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
PS Claim 1; SEQ ID NO 372; 241pp; English.
XX
CC The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
```

CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 12; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.3e-164;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGCGGAGGAGAGCCCTCTCTGACGCGCAGCCGCGCCGACCCACCATGGCCACAGTT 60
DB 1 ACCGCGGAGGAGAGCCCTCTCTGACGCGCAGCCGCGCCGACCCACCATGGCCACAGTT 60
QY 61 CAGCAGCTCGAAGGAGAGTGGCGCTGTGGAGCAGCAAAAGGCTTTGATGAATACATGAAG 120
DB 61 CAGCAGCTCGAAGGAGAGTGGCGCTGTGGAGCAGCAAAAGGCTTTGATGAATACATGAAG 120
QY 121 GAGCTAGGAGTGGGAATAGCTTTGGGAAAAATGGCGCAATGGCCAGCCAGATTGTATC 180
DB 121 GAGCTAGGAGTGGGAATAGCTTTGGGAAAAATGGCGCAATGGCCAGCCAGATTGTATC 180
QY 181 ATCACTTGTGATGTTAAACCTCACCATAAAAACTGAGAGCACTTTGAAAAACAACAG 240
DB 181 ATCACTTGTGATGTTAAACCTCACCATAAAAACTGAGAGCACTTTGAAAAACAACAG 240
QY 241 TTTTCTGTACCTGGGAGAGTGTGAAGAAACACACAGCTGTGCGAGAAACTCAG 300
DB 241 TTTTCTGTACCTGGGAGAGTGTGAAGAAACACACAGCTGTGCGAGAAACTCAG 300
QY 301 ACTGTCTGCAACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGTGGGATGGGAAGAA 360
DB 301 ACTGTCTGCAACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGTGGGATGGGAAGAA 360
QY 361 AGCAACAATAAGAAAAATTGAAAGATGGGAAATTAGTGGTGGAGTGTGTCATGAACAAT 420
DB 361 AGCAACAATAAGAAAAATTGAAAGATGGGAAATTAGTGGTGGAGTGTGTCATGAACAAT 420
QY 421 GTCACTGTCTCGGATCTATGAAAAGTAGAATAAATTCATCATCATCTTCATCTGGACAG 480
DB 421 GTCACTGTCTCGGATCTATGAAAAGTAGAATAAATTCATCATCATCTTCATCTGGACAG 480
QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
DB 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
QY 541 CTTTCTTTTCTCAATCTGTGTTCAATTAATCTTTATCAATAAATTTTACATGAGCTAT 600
DB 541 CTTTCTTTTCTCAATCTGTGTTCAATTAATCTTTATCAATAAATTTTACATGAGCTAT 600
QY 601 TTCAAGTGTGTGATTAATAGGATCATCCCTTTGGTTTAAATAAATGTTGTTG 660
DB 601 TTCAAGTGTGTGATTAATAGGATCATCCCTTTGGTTTAAATAAATGTTGTTG 660

QY 661 CT 662
DB 661 CT 662
RESULT 6
ADN03852
ID ADN03852 standard; cDNA; 662 BP.
XX
AC ADN03852;
XX 01-JUL-2004 (first entry)
XX Antipsoriatic cDNA sequence #125.
DE ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
KW Homo sapiens.
OS WO2004028479-A2.
PN 08-APR-2004.
PD 25-SEP-2003; 2003WO-US030907.
XX 25-SEP-2002; 2002US-0414006P.
XX (GETH) GENENTECH INC.
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
DR WPI; 2004-305105/28.
DR P-PSDB; ADN03853.
XX New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.
XX Claim 1; SEQ ID NO 246; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 12; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.3e-164;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGCGGAGGAGAGCCCTCTCTGACGCGCAGCCGCGCCGACCCACCATGGCCACAGTT 60
DB 1 ACCGCGGAGGAGAGCCCTCTCTGACGCGCAGCCGCGCCGACCCACCATGGCCACAGTT 60
QY 61 CAGCAGCTCGAAGGAGAGTGGCGCTGTGGAGCAGCAAAAGGCTTTGATGAATACATGAAG 120
DB 61 CAGCAGCTCGAAGGAGAGTGGCGCTGTGGAGCAGCAAAAGGCTTTGATGAATACATGAAG 120
QY 121 GAGCTAGGAGTGGGAATAGCTTTGGGAAAAATGGCGCAATGGCCAGCCAGATTGTATC 180
DB 121 GAGCTAGGAGTGGGAATAGCTTTGGGAAAAATGGCGCAATGGCCAGCCAGATTGTATC 180
QY 181 ATCACTTGTGATGTTAAACCTCACCATAAAAACTGAGAGCACTTTGAAAAACAACAG 240
DB 181 ATCACTTGTGATGTTAAACCTCACCATAAAAACTGAGAGCACTTTGAAAAACAACAG 240
QY 241 TTTTCTGTACCTGGGAGAGTGTGAAGAAACACACAGCTGTGCGAGAAACTCAG 300
DB 241 TTTTCTGTACCTGGGAGAGTGTGAAGAAACACACAGCTGTGCGAGAAACTCAG 300

QY 301 ACTGCTGCAACTTTACAGATGGTCAATTTGGTTTCAGCATCAGGAGCTGGGATGGGAAGAA 360
 Db |||||
 QY 301 ACTGCTGCAACTTTACAGATGGTCAATTTGGTTTCAGCATCAGGAGCTGGGATGGGAAGAA 360
 Db |||||
 QY 361 AGCAACAATAACAAGAAAATTGAAGATGGGAATTTAGTGGTGGAGTGTGTCTATGAACAAT 420
 Db |||||
 QY 361 AGCAACAATAACAAGAAAATTGAAGATGGGAATTTAGTGGTGGAGTGTGTCTATGAACAAT 420
 Db |||||
 QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAATTCATCATCACTTTGGACAG 480
 Db |||||
 QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAATTCATCATCACTTTGGACAG 480
 Db |||||
 QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAATCTCCATACGTGTTCTTT 540
 Db |||||
 QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAATCTCCATACGTGTTCTTT 540
 Db |||||
 QY 541 CTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600
 Db |||||
 QY 541 CTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600
 Db |||||
 QY 601 TTCAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTTAAATAAATGTTGTTGTG 660
 Db |||||
 QY 601 TTCAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTTAAATAAATGTTGTTGTG 660
 Db |||||
 QY 661 CT 662
 Db |||||
 QY 661 CT 662
 Db |||||

RESULT 7

AD019263

ID AD019263 standard; cDNA; 662 BP.

AC

XX

AD019263;

XX

12-AUG-2004 (first entry)

XX

Human PRO polynucleotide #98.

XX

Human; PRO; gene; ss; immune related disorder;
 systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
 vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 renal disease; demyelinating disease; central nervous system;
 peripheral nervous system; demyelinating polyneuropathy;
 Guillain-Barre syndrome;
 chronic inflammatory demyelinating polyneuropathy.

Homo sapiens.

XX

WO2004043361-A2.

XX

27-MAY-2004.

XX

06-NOV-2003; 2003WO-US035268.

XX

08-NOV-2002; 2002US-0425235P.

XX

(GETH) GENENTECH INC.

XX

Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;

PI Wood WI, Wu ID;

XX

WPI; 2004-420067/39.

XX

P-PSDB; AD019264.

XX

Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86398 useful for
 treating an immune related disorder such as systemic lupus erythematosus,
 rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 spondyloarthritis.

XX

PS Claim 1; SEQ ID NO 204; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides
 encoding them. The polypeptides and polynucleotides are useful for
 treating and diagnosing immune related disorders in mammals. The immune
 related disorders include systemic lupus erythematosus, rheumatoid
 arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 mellitus, immune-mediated renal disease, demyelinating diseases of the
 central or peripheral nervous system, demyelinating polyneuropathy,
 Guillain-Barre syndrome and chronic inflammatory demyelinating
 polyneuropathy. This sequence represents a human PRO polynucleotide of
 the invention.

SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 12; Length 662;

Best Local Similarity 100.0%; Pred. No. 1.3e-164;

Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGCGGACGAGACCCCTCTCTGACCGCCAGCCGCGCCGACCCACCATGCCACAGTT 60

Db |||||

1 ACCGCGGACGAGACCCCTCTCTGACCGCCAGCCGCGCCGACCCACCATGCCACAGTT 60

QY 61 CAGCAGCTGGGAAGAGATGGCGCTGGTGACAGCAAGGCTTTGATGAATACATGAAG 120

Db |||||

61 CAGCAGCTGGGAAGAGATGGCGCTGGTGACAGCAAGGCTTTGATGAATACATGAAG 120

QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAATGGCGCAATGGCGCAAGCAGATTGTATC 180

Db |||||

121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAATGGCGCAATGGCGCAAGCAGATTGTATC 180

QY 181 ATCACTTGTGATGTTAAACCTCACCAATAAACTGAGAGACATTTGAAACCAACACAG 240

Db |||||

181 ATCACTTGTGATGTTAAACCTCACCAATAAACTGAGAGACATTTGAAACCAACACAG 240

QY 241 TTTTCTGTACCTCGGAGAGAGATTTGAAGAAAACACAGCTGTATGGCAGAAAAACTCAG 300

Db |||||

241 TTTTCTGTACCTCGGAGAGAGATTTGAAGAAAACACAGCTGTATGGCAGAAAAACTCAG 300

QY 301 ACTGTCCTCAACTTTTACAGATGGTGCATTTGTTTACAGATCAGGAGTGGATGGGAAGAA 360

Db |||||

301 ACTGTCCTCAACTTTTACAGATGGTGCATTTGTTTACAGATCAGGAGTGGATGGGAAGAA 360

QY 361 AGCAACAATAACAAGAAAATTGAAGATGGGAATTTAGTGGTGGAGTGTGTCTATGAACAAT 420

Db |||||

361 AGCAACAATAACAAGAAAATTGAAGATGGGAATTTAGTGGTGGAGTGTGTCTATGAACAAT 420

QY 421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAATTCATCATCACTTTGGACAG 480

Db |||||

421 GTCACCTGTACTCGGATCTATGAAAAGTAGAATAAATTCATCATCACTTTGGACAG 480

QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAATCTCCATCTCTTTCTTT 540

Db |||||

481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAATCTCCATCTCTTTCTTT 540

QY 541 CTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600

Db |||||

541 CTTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 600

QY 601 TTCAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTTAAATAAATGTTGTTGTG 660

Db |||||

601 TTCAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTTAAATAAATGTTGTTGTG 660

QY 661 CT 662

Db |||||

661 CT 662

XX

RESULT 8

ADP13321

ID ADP13321 standard; DNA; 662 BP.

XX ADP13321;
 XX 26-AUG-2004 (first entry)
 XX Renal cell carcinoma differentially expressed gene #57.
 DE ds; diagnosis; non-blood disease; solid tumor; gene expression;
 KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
 KW head/neck cancer; differential expression.
 XX Homo sapiens.
 XX WO2004048933-A2.
 XX 10-JUN-2004.
 XX 21-NOV-2003; 2003WO-US037481.
 XX 21-NOV-2002; 2002US-0427982P.
 XX 03-APR-2003; 2003US-0459782P.
 XX (AMHP) WYETH.
 XX (TWIN/) TWINE N C.
 XX (BURC/) BURCZYNSKI M E.
 XX (TREP/) TREPICCHIO W L.
 XX (DORN/) DORNER A.
 XX (STOV/) STOVER J A.
 XX (SLOW/) SLOWI D K.
 XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
 PI Sloni DK;
 XX WPI; 2004-460799/43.
 XX Diagnosing non-blood disease such as solid tumor, involves comparing
 PT differential expression profile of specific genes in peripheral blood
 PT sample of subject with reference expression profile of specific genes.
 XX Disclosure; SEQ ID NO 57; 350pp; English.
 XX The invention relate to a method of diagnosing (M1) non-blood disease
 CC such as solid tumor by providing peripheral blood sample of human having
 CC non-blood disease, and comparing an expression profile of specific genes
 CC in the peripheral blood sample to reference expression profile of the
 CC genes, where each of the genes is differentially expressed in peripheral
 CC blood mononuclear cells (PBMCs) of patients having the disease as
 CC compared to PBMCs of normal humans. The method is useful for diagnosing
 CC non-blood disease such as solid tumor. The solid tumor is chosen from
 CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
 CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
 CC sample is a whole blood sample (claimed). (M1) is useful for identifying
 CC genes that are differentially expressed in peripheral blood samples
 CC isolated at different stages of progression, development or treatment of
 CC RCC and/or other solid tumors. This sequence corresponds to a gene that
 CC is differentially expressed and detected by the method of the invention.
 CC (Note: this sequence is not given as part of the printed specification
 CC but was obtained from WIPO in electronic format at
 CC ftp.wipo./pub/published_pct_sequences).
 XX Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 662; DB 12; Length 662;
 Best Local Similarity 100.0%; Pred. No. 1.3e-164;
 Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACCGCCGACGACACCCCTCTCTGACGCGCAGCCGCCGCCACCCACCATGGCCACAGTT 60
 DB 1 ACCGCCGACGACACCCCTCTCTGACGCGCAGCCGCCGCCACCCACCATGGCCACAGTT 60
 QY 61 CAGCAGCTGGAGGAGATGGCGCTCTGGCAGCAAGAGGCTTGATCAATACATGAG 120
 DB 61 CAGCAGCTGGAGGAGATGGCGCTCTGGCAGCAAGAGGCTTGATCAATACATGAG 120

QY 121 GAGCTAGGAGTGGGAATAGCTTTTGGCAAAAAATGGCGCAATGGCCAAAGCCAGATTGTATC 180
 DB 121 GAGCTAGGAGTGGGAATAGCTTTTGGCAAAAAATGGCGCAATGGCCAAAGCCAGATTGTATC 180
 QY 181 ATCAGCTTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACTTTTGAAGAAACCAACACAG 240
 DB 181 ATCAGCTTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACTTTTGAAGAAACCAACACAG 240
 QY 241 TTTTCTTGTACCTCGGAGAGAGTGTGAAGAAACCAACAGCTGATGCGCAAGAAAACCTCAG 300
 DB 241 TTTTCTTGTACCTCGGAGAGAGTGTGAAGAAACCAACAGCTGATGCGCAAGAAAACCTCAG 300
 QY 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTACAGATCAGAGTGGGATGGGAAGGAA 360
 DB 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTACAGATCAGAGTGGGATGGGAAGGAA 360
 QY 361 AGCACAATAACAAGAAATTTGAAGATGGGAAATTTAGTGTGGAGTGTGTCTATGAACAAT 420
 DB 361 AGCACAATAACAAGAAATTTGAAGATGGGAAATTTAGTGTGGAGTGTGTCTATGAACAAT 420
 QY 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTGGACAG 480
 DB 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTGGACAG 480
 QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATACACTGTTCTTT 540
 DB 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATACACTGTTCTTT 540
 QY 541 CTTTCTTTTTCATTACTGTGTTCAATATCTTATCATATAAACATTTTACATGCAGCTAT 600
 DB 541 CTTTCTTTTTCATTACTGTGTTCAATATCTTATCATATAAACATTTTACATGCAGCTAT 600
 QY 601 TTCAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
 DB 601 TTCAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
 QY 661 CT 662
 DB 661 CT 662

RESULT 9
 ADR24747
 ID ADR24747 standard; DNA; 662 BP.
 XX ADR24747;
 XX 21-OCT-2004 (first entry)
 DE Breast cancer prognosis marker #608.
 KW ds; breast cancer; prognosis; gene expression; diagnosis.
 OS Homo sapiens.
 XX WO2004065545-A2.
 XX 05-AUG-2004.
 XX 15-JAN-2004; 2004WO-US001100.
 XX 15-JAN-2003; 2003US-00342887.
 XX (ROSE-) ROSETTA INPHARMATICS LLC.
 XX (NECA-) NETHERLANDS CANCER INST.
 XX Van't Veer LJ, He Y;
 XX WPI; 2004-593473/57.
 XX Classifying a breast cancer patient according to prognosis comprises
 PT determining the similarity between the level of expression of each of

PT five genes in a cell sample taken from patient, to control levels.
XX
XX
PS Disclosure; SEQ ID NO 608; 226pp; English.
XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
XX Sequence 662 BP: 210 A: 128 C: 150 G: 174 T: 0 U: 0 Other:

Query Match	100.08;	Score 662;	DB 13;	Length 662;
Best Local Similarity	100.08;	Prod. No. 1.3e-164;		
Matches 662;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACCGCCGACGACAGCCCTCTCTGCA	CGCCGCGCCGACCCACCATGCGCCACAGTT	60
Db				
Qy	1	ACCGCCGACGACAGCCCTCTCTGCA	CGCCGCGCCGCGCCGACCCACCATGCGCCACAGTT	60
Db				
Qy	61	CAGCAGCTGGAGGAAGATGCGCCTG	TGGACAGCAAAAGGCTTTTGATGAATACATGAAG	120
Db				
Qy	61	CAGCAGCTGGAGGAAGATGCGCCTG	TGGACAGCAAAAGGCTTTTGATGAATACATGAAG	120
Db				
Qy	121	GAGCTAGAGTGGAAATAGCTTTTGG	CAAAAATGCGGCCAATGGCCACAGCCAGATTGTATC	180
Db				
Qy	121	GAGCTAGAGTGGAAATAGCTTTTGG	CAAAAATGCGGCCAATGGCCACAGATTGTATC	180
Db				
Qy	181	ATCACTTGTGATGTTAAAAACCTCA	CACATAAAACCTTGAGAGCACCTTGAACAACAACACAG	240
Db				
Qy	181	ATCACTTGTGATGTTAAAAACCTCA	CACATAAAACCTTGAGAGCACCTTGAACAACAACAACAG	240
Db				
Qy	241	TTTTTCTGTACCTGGGAGAGAAAGT	TGAAGAAAACCAAGCTGATGGCAGAAAAA	300
Db				
Qy	241	TTTTTCTGTACCTGGGAGAGAAAGT	TGAAGAAAACCAAGCTGATGGCAGAAAAA	300
Db				
Qy	301	ACTGTCGCAACTTACAGATGGTGCA	TTGGTTTACGATCAGGAGTGGGATGGGAAGAA	360
Db				
Qy	301	ACTGTCGCAACTTACAGATGGTGCA	TTGGTTTACGATCAGGAGTGGGATGGGAAGAA	360
Db				
Qy	361	AGCAACAATAACAAGAAAATTCGA	AGATGGGAAATAGTGGTGGAGTGTGTCAATGAACAAT	420
Db				
Qy	361	AGCAACAATAACAAGAAAATTCGA	AGATGGGAAATAGTGGTGGAGTGTGTCAATGAACAAT	420
Db				
Qy	421	GTCACCTGTACTCGGATCTATGAAA	AAAGTAGAATAAAAAATTCATCATCCTTTGGACAG	480
Db				
Qy	421	GTCACCTGTACTCGGATCTATGAAA	AAAGTAGAATAAAAAATTCATCATCCTTTGGACAG	480
Db				
Qy	481	GAGTTAATAAGAGATGACCAAGCT	CAAGTTCAGTTCAGGCAATCTCCATCTGTTCTTT	540
Db				
Qy	481	GAGTTAATAAGAGAGATGACCAAGCT	CAAGTTCAGTTCAGGCAATCTCCATCTGTTCTTT	540
Db				
Qy	541	CTTTTTTTTTTTCATTACGTGTTC	AAATATCTTTTATCATAAACATTTTACATGCAGCTAT	600
Db				
Qy	541	CTTTTTTTTTTTCATTACGTGTTC	AAATATCTTTTATCATAAACATTTTACATGCAGCTAT	600
Db				
Qy	601	TTCAAAGTGTGTGGATTAATTAGG	ATCATCCCTTTGGTTTAATAAATGTTGTTGTG	660
Db				
Qy	601	TTCAAAGTGTGTGGATTAATTAGG	ATCATCCCTTTGGTTTAATAAATGTTGTTGTG	660
Db				
Qy	661	CT	662	
Db				
Qy	661	CT	662	
Db				

RESULT 10
ACN38822
ID ACN38822

XX	ACN38822;
XX	18-NOV-2004 (first entry)
XX	Tumour-associated antigenic target (TAT) cDNA DNA325115, SEQ ID NO:2575.
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX	tumour; diagnosis; cell proliferative disorder; breast cancer;
XX	colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX	central nervous system cancer; bladder cancer; pancreatic cancer;
XX	cervical cancer; melanoma; leukaemia; hybridisation probe;
XX	chromosome identification; chromosome mapping; gene mapping;
XX	gene therapy; cytostatic; gene; ss.
OS	Homo sapiens.
XX	WO2004030615-A2.
XX	15-APR-2004.
XX	29-SEP-2003; 2003WO-US028547.
XX	02-OCT-2002; 2002US-0414971P.
XX	(GETH) GENENTECH INC.
XX	Wu TD, Zhang Z, Zhou Y;
PI	WPI; 2004-347921/32.
DR	P-PSDB; ABM80997.
XX	New tumor-associated antigenic target polypeptides and nucleic acids,
XX	useful in preparing a medicament for treating or detecting a
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT	prostate cancer or tumor.
XX	Claim 1; SEQ ID NO 2575; 7273pp; English.
XX	The invention relates to human tumour-associated antigenic target (TAT)
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are
CC	overexpressed in cancer tissues compared to normal tissues, and may thus
CC	serve as effective targets for the diagnosis and treatment of cancer in
CC	mammals. The invention also relates to nucleic acid and polypeptide
CC	sequences at least 80% identical to the TAT nucleic acids and
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC	TAT polypeptide; and methods and compositions for the treatment or
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC	antibodies, antagonists, binding molecules and compositions are useful
CC	for diagnosing or treating a cell proliferative disorder associated with
CC	increased TAT expression, particularly cancers such as breast cancer,
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC	used as hybridisation probes, in chromosome and gene mapping, in
CC	chromosome identification and in gene therapy. The present sequence
CC	represents a TAT nucleic acid of the invention
XX	
XX	Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;
XX	
XX	Query Match 100.0%; Score 662; DB 13; Length 662;
XX	Best Local Similarity 100.0%; Pred. No. 1.3e-164;
XX	Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ACCGCCGACGACAGCCCTCTCTGCAGCCAGCCGCCGCCGCCACCATGGCCACAGTT 60
Dd	1 ACCGCCGACGACAGCCCTCTCTGCAGCCAGCCGCCGCCGCCACCATGGCCACAGTT 60
Qy	61 CAGCAGCTGGAAGAGATGGCGCTGTGTGACAGCAGCAAGCGTTTGATGATCATGAAG 120
Dd	61 CAGCAGCTGGAAGAGATGGCGCTGTGTGACAGCAGCAAGCGTTTGATGATCATGAAG 120

```
QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAAATGGGCGCAATGGCCAAAGCCAGATTGTATC 180
DB |||||||
QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAAATGGGCGCAATGGCCAAAGCCAGATTGTATC 180
DB |||||||
QY 181 ATCACTTGTGATGTTAAACCTTCCATATAAACTGAGGACACTTTGAAACACACAG 240
DB |||||||
QY 181 ATCACTTGTGATGTTAAACCTTCCATATAAACTGAGGACACTTTGAAACACACAG 240
DB |||||||
QY 241 TTTTCTGTACCTCGGAGAGAGTTTGAAGAACACACAGCTGATGGCAAAAACTCAG 300
DB |||||||
QY 301 ACTGCTGCAACTTTACAGATGTCATTTGGTTTCCAGTCAGGATGGGATGGGAAGGAA 360
DB |||||||
QY 301 ACTGCTGCAACTTTACAGATGTCATTTGGTTTCCAGTCAGGATGGGATGGGAAGGAA 360
DB |||||||
QY 361 AGCACATAACGAAGAAATTTGAAGATGGAATTTAGTGTGAGTGTGTCATGAACAAT 420
DB |||||||
QY 361 AGCACATAACGAAGAAATTTGAAGATGGAATTTAGTGTGAGTGTGTCATGAACAAT 420
DB |||||||
QY 421 GTCACCTGTACTCGGATCTATGAAAGTAGAATAAAAAATTCATCATCACTTTGGACAG 480
DB |||||||
QY 481 GAGTTAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTTTTCTTT 540
DB |||||||
QY 481 GAGTTAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCACTTTTCTTT 540
DB |||||||
QY 541 CTTTCTTTTTCATCTACTGTGTTCAATTTCTTATCATATAACATTTTACATGCACTAT 600
DB |||||||
QY 601 TTCAAAGTGTGTTGGAATTAATAGGATCATCCCTTTGTTTAAATAAATGTTTGTG 660
DB |||||||
QY 661 CT 662
DB ||
QY 661 CT 662
```

RESULT 11

ADP54337
ID ADP54337 standard; cDNA; 662 BP.

AC ADP54337;

DT 18-NOV-2004 (first entry)

DE Human PRO cDNA sequence SEQ ID NO:313.

KW human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antirheumatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antihemetic; antihydroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy; gene; ss.

OS Homo sapiens.

PN WO2004039956-A2.

PD 13-MAY-2004.

PF 28-OCT-2003; 2003WO-US034381.

PR 29-OCT-2002; 2002US-0422472P.

PA (GETH) GENENTECH INC.

PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

PI Wood WI, Wu TD;

XX WPI; 2004-376182/35.

DR P-PSDB; ADP54338.

XX New PRO polynucleotides and polypeptides, useful in diagnosing

PT and treating an immune related disease, e.g. systemic lupus

PT erythematous, rheumatoid arthritis, diabetes mellitus or asthma and in

XX stimulating an immune response.

PS Claim 2; SEQ ID NO 313; 3009pp; English.

XX The present invention describes an isolated PRO nucleic acid (I). Also
CC described: (1) a vector comprising (I); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antirheumatic, antidiabetic, antiinflammatory, antipsoriatic,
CC haemostatic, antihydroid, CNS, dermatological, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO nucleotide sequence from the present invention.

SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 13; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.3e-164;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGCGGAGCGAGACCCCTCTCTGCGCGCCGCGCCGCCGCCACCCAGCCAGTT 60

DB 1 ACCGCGGAGCGAGACCCCTCTCTGCGCGCCGCGCCGCCGCCACCCAGCCAGTT 60

QY 61 CAGCAGCTGGAAAGGAGATGGCGCTGTGGAGCAGCAAGGCTTTGATGAATACATGAAG 120

DB 61 CAGCAGCTGGAAAGGAGATGGCGCTGTGGAGCAGCAAGGCTTTGATGAATACATGAAG 120

QY 121 GAGCTAGGATGGGAATAGCTTTGCGAAAAATGGGCGCAATGGCCAGCAGATTGTATC 180

DB 121 GAGCTAGGATGGGAATAGCTTTGCGAAAAATGGGCGCAATGGCCAGCAGATTGTATC 180

QY 181 ATCACTTGTGATGTTAAACCTCACCATAAAATGAGACACTTTGAAAACACACAG 240

DB 181 ATCACTTGTGATGTTAAACCTCACCATAAAATGAGACACTTTGAAAACACACAG 240

QY 241 TTTTCTTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGTAGTGGCAAAAACCTCAG 300

DB 241 TTTTCTTGTACCTCGGAGAGAGTTTGAAGAAACACACAGCTGTAGTGGCAAAAACCTCAG 300

QY 301 ACTGTCTGCAACTTTTACAGATGGTGCATTTGGTTTCCAGCATCAGGATGGGATGGGAAGGAA 360

DB 301 ACTGTCTGCAACTTTTACAGATGGTGCATTTGGTTTCCAGCATCAGGATGGGATGGGAAGGAA 360

QY 361 AGCACATAACGAAGAAATTTGAAGATGGAATTTAGTGTGAGTGTGTCATGAACAAT 420

DB 361 AGCACATAACGAAGAAATTTGAAGATGGAATTTAGTGTGAGTGTGTCATGAACAAT 420

QY 421 GTCACTGTACTCGGATCTATGAAAAGTAGAATAAAATTCATCATCATTGGACAG 480
Db 421 GTCACTGTACTCGGATCTATGAAAAGTAGAATAAAATTCATCATCATTGGACAG 480
QY 481 GAGTTAAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
Db 481 GAGTTAAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
QY 541 CTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATATAACATTTTACATGAGCTAT 600
Db 541 CTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATATAACATTTTACATGAGCTAT 600
QY 601 TTCAAAGTGTGTTGGATTAAATTAGATCATCCCTTTGGTTAATAATAAATGTTTGTG 660
Db 601 TTCAAAGTGTGTTGGATTAAATTAGATCATCCCTTTGGTTAATAATAAATGTTTGTG 660
QY 661 CT 662
Db 661 CT 662

RESULT 12

ADRS52981
ID ADRS52981 standard; DNA; 662 BP.

XX ADRS52981;

XX 18-NOV-2004 (first entry)

XX Drug therapy altered expressed gene #332.

XX drug activity monitoring; expression profile; gene expression;
KW peripheral blood sample; peripheral blood mononuclear cell; drug therapy;
KW CCI-779; immunosuppressant; rapamycin; mammalian target of rapamycin;
KW mTOR; ds.

XX Homo sapiens.

XX WO2004072265-A2.

XX 26-AUG-2004.

XX 11-FEB-2004; 2004WO-US004118.

XX 11-FEB-2003; 2003US-0446133P.

PR 03-APR-2003; 2003US-0459782P.

PR 23-JAN-2004; 2004US-0538246P.

XX (AMHP) WYETH.

PA (BURC/) BURCZYNSKI M.

PA (TWIN/) TWINE N.

PA (DORN/) DORNER A. J.

PA (TREP/) TREPICCHIO W. L.

XX Burczynski M, Twine N, Dorner AJ, Trepicchio WL;
PI WPI; 2004-642301/62.

DR Monitoring drug activities in vivo comprises comparing an expression

PT profile of a gene in a peripheral blood sample of a patient before and
PT after drug therapy.

XX Disclosure; SEQ ID NO 332; 136pp; English.

XX The invention relates to a method of monitoring drug activities in vivo
CC by comparing an expression profile of at least one gene in a peripheral
CC blood sample of a patient to a reference expression profile of the at
CC least one gene, where the at least one gene is differentially expressed
CC in peripheral blood mononuclear cells (PBMCs) of patients who have a non-
CC blood disease and are subjected to a drug therapy as compared to PBMCs
CC isolated from the patient before the drug therapy, and where the patient
CC has the non-blood disease and is being treated by the drug therapy. The

CC method, kit, and nucleic acid array are useful for monitoring drug
CC activities in vivo. The drug is especially CCI-779, an ester analogue of
CC the immunosuppressant rapamycin which is a potent inhibitor of the
CC mammalian target of rapamycin (mTOR). This sequence represents a gene
CC expressed in PBMC altered by the drug therapy. (Note: this sequence does
CC no form part of the printed specification but was obtained in electronic
CC format from WIPO at ftp.wipo.int/pub/published_pct_sequences/).

SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 13; Length 662;
Best Local Similarity 100.0%; Pred. No. 1.3e-164;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGCCGACGACAGACCCCTCTCTGCACGCCAGCCGCCGCCACCCACCCAGTTCAGTT 60
Db 1 ACCGCCGACGACAGACCCCTCTCTGCACGCCAGCCGCCGCCACCCACCCAGTTCAGTT 60
QY 61 CAGCAGCTGGGAAGAGATGGCGCTGCTGGACAGCAAGGCTTTGATGAATACATGAAG 120
Db 61 CAGCAGCTGGGAAGAGATGGCGCTGCTGGACAGCAAGGCTTTGATGAATACATGAAG 120
QY 121 GAGCTAGAGTGGGAATAGCTTTTGGAAAAATGGCGCAATGGCCAGCAGATTGTATC 180
Db 121 GAGCTAGAGTGGGAATAGCTTTTGGAAAAATGGCGCAATGGCCAGCAGATTGTATC 180
QY 181 ATCACTTGTGATGTTAAAAAGCTCACCATAAAAACTGAGAGCAGCTTTGAAAAACAACAG 240
Db 181 ATCACTTGTGATGTTAAAAAGCTCACCATAAAAACTGAGAGCAGCTTTGAAAAACAACAG 240
QY 241 TTTTCTTGTACCTCGGAGAGAGTGTGAAGAAACACAGCTGTATGGCAGAAAAACTCAG 300
Db 241 TTTTCTTGTACCTCGGAGAGAGTGTGAAGAAACACAGCTGTATGGCAGAAAAACTCAG 300
QY 301 ACTGCTGCAACTTTACAGATGCTGCATTTGGTTTCAGATCAGGATGGGATGGGAAGGA 360
Db 301 ACTGCTGCAACTTTACAGATGCTGCATTTGGTTTCAGATCAGGATGGGATGGGAAGGA 360
QY 361 AGCAATAACAAGAAAAATGAAGATGGGAAATTTAGTGGTGGAGTGTGTATGAACAAT 420
Db 361 AGCAATAACAAGAAAAATGAAGATGGGAAATTTAGTGGTGGAGTGTGTATGAACAAT 420
QY 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTTGGACAG 480
Db 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCTTTGGACAG 480
QY 481 GAGTTAAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
Db 481 GAGTTAAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
QY 541 CTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATATAACATTTTACATGAGCTAT 600
Db 541 CTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATATAACATTTTACATGAGCTAT 600
QY 601 TTCAAAGTGTGTTGGATTAAATTAGATCATCCCTTTGGTTAATAATAAATGTTTGTG 660
Db 601 TTCAAAGTGTGTTGGATTAAATTAGATCATCCCTTTGGTTAATAATAAATGTTTGTG 660
QY 661 CT 662
Db 661 CT 662

RESULT 13

ADP25373
ID ADP25373 standard; cDNA; 662 BP.

XX AC ADP25373;

XX DT 18-NOV-2004 (first entry)

XX PRO polypeptide encoding cDNA SEQ ID NO:487.

ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

Unidentified.

WO2004041170-A2.

21-MAY-2004.

30-OCT-2003; 2003WO-US034312.

01-NOV-2002; 2002US-0423394P.

(GETH) GENENTECH INC.

Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI; Wu TD;

WPI; 2004-419628/39.

P-PSDB; ADP25374.

New PRO polypeptides and polynucleotides, useful for treating e.g. erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.

Claim 1; SEQ ID NO 487; 2940pp; English.

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplant-associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.

Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match 100.0%; Score 662; DB 13; Length 662;

Best Local Similarity 100.0%; Pred. No. 1.3e-164;

Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGCGAGCAGACCCCTCTGACGCGCAGCCGCCGCCACCCACCCAGCAGTT 60

DB 1 ACCGCGAGCAGACCCCTCTGACGCGCAGCCGCCGCCACCCACCCAGCAGTT 60

QY 61 CAGCAGCTGGAGAGAGATGGCCCTCTGAGCAGCAAGCAAGCTTTCATGAATACATGAAG 120

DB 61 CAGCAGCTGGAGAGAGATGGCCCTCTGAGCAGCAAGCAAGCTTTCATGAATACATGAAG 120

QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAGGATTTGATTC 180

Db 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAGGATTTGATTC 180

QY 181 ATCACTTGTGATGTAATAAACTCCACCATATAAACTGAGAGCAGCTTTGAAAAACAACACAG 240

Db 181 ATCACTTGTGATGTAATAAACTCCACCATATAAACTGAGAGCAGCTTTGAAAAACAACACAG 240

QY 241 TTTTCTGTACCCCTGGGAGAGAGTTTGAAGAAAACAAGCTGATGGCAGAAAACTCAG 300

Db 241 TTTTCTGTACCCCTGGGAGAGAGTTTGAAGAAAACAAGCTGATGGCAGAAAACTCAG 300

QY 301 ACTGCTGCAACTTTTACAGATGTCATTTGAGTTCAGCATCAGAGTGGGATGGGAAGGAA 360

Db 301 ACTGCTGCAACTTTTACAGATGTCATTTGAGTTCAGCATCAGAGTGGGATGGGAAGGAA 360

QY 361 AGCAACAATAAACAAGAAATTTGAAGATGGGAAATTTAGTGGTGGAGTGTCTCATGAACAAT 420

Db 361 AGCAACAATAAACAAGAAATTTGAAGATGGGAAATTTAGTGGTGGAGTGTCTCATGAACAAT 420

QY 421 GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAATTTCCATCATCATCTTGGACAG 480

Db 421 GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAATTTCCATCATCATCTTGGACAG 480

QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTCTTT 540

Db 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTCTTT 540

QY 541 CTTTCTTTTTCATTAATCTGTTCAATTTATCTTTATCATAAAACATTTTACATGCAGCTAT 600

Db 541 CTTTCTTTTTCATTAATCTGTTCAATTTATCTTTATCATAAAACATTTTACATGCAGCTAT 600

QY 601 TTCAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTAATAATAATGTTGTTG 660

Db 601 TTCAAGTGTGTGGATTAATTTAGGATCATCCCTTTGGTTAATAATAATGTTGTTG 660

QY 661 CT 662

Db 661 CT 662

RESULT 14

ADR99018

ID ADR99018 standard; DNA; 662 BP.

XX AC ADR99018;

XX AC 02-DEC-2004 (first entry)

XX DE Fatty acid binding protein 5 (psoriasis-associated), FABP5, DNA.

XX KW Cytostatic; breast cancer; cancer; human; gene; ds;

XX KW Fatty acid binding protein 5; psoriasis-associated; FABP5.

XX OS Homo sapiens.

XX PN WO2004078035-A2.

XX PD 16-SEP-2004.

XX PF 27-FEB-2004; 2004WO-US007268.

XX PR 28-FEB-2003; 2003US-0450655P.

XX PA (FARB) BAYER PHARM CORP.

XX PI Eveleigh D, Bigwood D;

XX DR WPI; 2004-653556/63.

XX DR P-PSDB; ADR99145.

XX DR REFSEQ; NM_001444.1.

XX PT Diagnosing breast cancer comprises comparing the level of expression of genes or gene products in a first biological sample taken from a patient

PT	with that in a normal patient sample.		
XX	Claim 2; SEQ ID NO 24; 53pp; English.		
CC	The present invention relates to a method (M1) for diagnosing breast cancer in a patient. The method comprises comparing the level of expression of one or more genes or gene products in a biological sample from the patient with that in a normal patient sample, where a difference in the gene expression in the first sample compared to that in the second sample is a diagnostic of the disease. Also claimed are: method (M2) for distinguishing between normal and disease tissues; method (M3) for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent; method (M4) for identifying a compound for treating breast cancer; and an array for distinguishing between normal and disease tissues comprising two or more probes corresponding to genes selected from ADR98995-ADR99121 or comprising two or more polypeptides selected from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995-ADR99121 and the gene products are polypeptides selected from ADR99122-ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are useful for distinguishing between normal and disease tissue. M3 is useful for monitoring the response of a breast cancer patient to treatment with an anti-cancer agent. M4 is useful for identifying a compound for treating breast cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fcp.wipo.int/pub/published_pct_sequences.		
XX	Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;		
SQ	Query Match 100.0%; Score 662; DB 13; Length 662; Best Local Similarity 100.0%; Pred. No. 1.3e-164; Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	ACCGCGGAGAGACCCCTCTGACGCGCCGCGCCGACCCACCATGCGCCACAGTT	60
DB	1		60
QY	61	CAGCAGCTGGAAGAGAGAGTGGCGCTGTGGACGACGAAAGGCTTTGATGATACATGAAG	120
DB	61		120
QY	121	GAGCTAGGAGTGGGAATAGCTTTGGGAAAATGGGCGCAATGGCCAGCAGATTGTATC	180
DB	121		180
QY	181	ATCAGCTGTGATGTTAAACCTCACCATAAAACCTGAGAGCATTGGAACACACAG	240
DB	181		240
QY	241	TTTTCTGTACCTGGAGAGAGTTTGAAGAAACACAGCTGATGGCAGAAAACCTCAG	300
DB	241		300
QY	301	ACTGCTGCAATTTACAGATGGTGATTTGGTTTACAGATCAGAGTGGGATGGGAAGAA	360
DB	301		360
QY	361	ACGCAATAACAGAAAATTGAAGATGGAATAGTGGTGGAGTGTCTATGACAT	420
DB	361		420
QY	421	GTCCCTGTACCTCGGATCTATGAAAAGTAGAATAAAATTCATCATCATTGGACAG	480
DB	421		480
QY	481	GAGTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATACGTCTTTT	540
DB	481		540
QY	541	CTTTTCTTTTCTACTGTTTCAATATCTTTATCAATAACATTTACATGCGAGCTAT	600
DB	541		600
QY	601	TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAATAAATGTTGTG	660

Db	601	TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAATAAATGTTGTG	660
QY	661	CT 662	
DB	661	CT 662	
RESULT 15			
ADR66234			
ID	ADR66234	standard; DNA; 662 BP.	
AC	ADR66234;		
XX	02-DEC-2004	(first entry)	
DE	Human prostatic carcinoma derived DNA SEQ ID 88 #2.		
XX	human; cytostatic; diagnosis; prostatic cancer;		
KW	differential expression analysis; ds.		
XX	Homo sapiens.		
PN	WO2004076614-A2.		
XX	10-SEP-2004.		
XX	22-FEB-2004; 2004WO-DE000433.		
PR	27-FEB-2003; 2003DE-01009985.		
PR	14-MAY-2003; 2003DE-01022134.		
XX	(HINZ/) HINZMANN B.		
PA	(DAHL/) DAHL E.		
PA	(ROSE/) ROSENTHAL A.		
PA	(HERM/) HERMANN K.		
PA	(PILA/) PILARSKY C.		
XX	Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pillarsky C, Specht T;		
PI	Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;		
PI	Xinzhong L, Staub E;		
XX	WPI; 2004-653386/63.		
XX	New nucleic acids, and encoded proteins, from prostatic cancer tissue,		
PT	useful for diagnosis, treatment and in screening for specific binding		
PT	agents.		
XX	Claim 1; Page 502; 1607pp; German.		
PS	This invention describes novel cytostatic polynucleotide and polypeptide		
CC	sequences which can be used in a method for diagnosing prostatic cancer		
CC	or the risk of developing prostatic cancer. Diagnosis is based on		
CC	determining over transcription or over expression of the sequences in		
CC	prostatic tissue. Screening for inhibitors of the sequences or detection		
CC	substances involves a binding assay, any compounds that bind are		
CC	selected, optionally after deconvolution of mixtures. Detection of a		
CC	predetermined minimum level of the reporter indicates the presence of		
CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,		
CC	short-interfering RNA or ribozymes; an organic molecule of molecular		
CC	weight below 5000, preferably 300, that binds to the polypeptide; an		
CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the		
CC	polypeptide, preferably humanised or human; an anti-idiotypic, non-human		
CC	(monoclonal) antibody directed against Ab or any of the above derivatised		
CC	with a reporter group, cell toxin, immunostimulatory molecules and/or		
CC	radioisotope. The polynucleotides are identified in human prostatic		
CC	cancer by differential expression analysis, using DNA microarrays,		
CC	between normal and tumorous tissues, with (over)expression being detected		
CC	by quantitative PCR. Analysis of prostatic cancer samples showed that		
CC	CD24 was upregulated in many of them. Sections of tissue, isolated from		
CC	prostatic cancer patients, or subjects at risk, were incubated		
CC	sequentially with anti-human CD4 murine monoclonal antibodies;		
CC	biotinylated second antibody; streptavidin-conjugated horseradish		

CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX

SQ Sequence 662 BP; 210 A; 128 C; 150 G; 174 T; 0 U; 0 Other;

Query Match		100.0%;	Score 662;	DB 13;	Length 662;
Best Local Similarity		100.0%;	Pred. No. 1.3e-164;		
Matches 662;	Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;
QY	1	ACCGCGCAGCAGACCCCTCTCTGACGCGAGCCCGCCGCAACCCACCATGGCCACAGTT	60		
DB	1	ACCGCGCAGCAGACCCCTCTCTGACGCGAGCCCGCCGCAACCCACCATGGCCACAGTT	60		
QY	61	CAGCAGCTGGAAGGAGATGGCGCTGGTGGACAGCAAGGCTTTGATGAATACATGAAG	120		
DB	61	CAGCAGCTGGAAGGAGATGGCGCTGGTGGACAGCAAGGCTTTGATGAATACATGAAG	120		
QY	121	GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATC	180		
DB	121	GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAAAGCCAGATTGTATC	180		
QY	181	ATCATTGTGTAGTGGTAAAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACACAG	240		
DB	181	ATCATTGTGTAGTGGTAAAAACCTCACATATAAACTGAGAGCACTTTGAAAAACAACACAG	240		
QY	241	TTTTCTTGTACCTGGGAGAGATTGGAAGAAACACAGCTGATGGGAGAAAACTCAG	300		
DB	241	TTTTCTTGTACCTGGGAGAGATTGGAAGAAACACAGCTGATGGGAGAAAACTCAG	300		
QY	301	ACTGCTGCAACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGTGGGATGGAAGGAA	360		
DB	301	ACTGCTGCAACTTTACAGATGGTGCATTGGTTTCAGCATCAGAGTGGGATGGAAGGAA	360		
QY	361	AGCACAATAACAGAAAAATTGAAGATGGGAAATTAGTGGTGGAGTGTGCATGAACAAT	420		
DB	361	AGCACAATAACAGAAAAATTGAAGATGGGAAATTAGTGGTGGAGTGTGCATGAACAAT	420		
QY	421	GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCACTTTGGACAG	480		
DB	421	GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCACTTTGGACAG	480		
QY	481	GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCTGTTCTTT	540		
DB	481	GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCTGTTCTTT	540		
QY	541	CTTTTTTTTTTCACTACTGTGTTCAATTAATCTTTATCATATAAACATTTTACATGCAGCTAT	600		
DB	541	CTTTTTTTTTTCACTACTGTGTTCAATTAATCTTTATCATATAAACATTTTACATGCAGCTAT	600		
QY	601	TTCAAAGTGTGTGGAATTAATAGGATCATCCCTTTGGTTAATAATAAATGTGTTTGTG	660		
DB	601	TTCAAAGTGTGTGGAATTAATAGGATCATCCCTTTGGTTAATAATAAATGTGTTTGTG	660		
QY	661	CT 662			
DB	661	CT 662			

Search completed: July 12, 2005, 18:01:42
Job time : 420.141 secs

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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 15:11:39 ; Search time 4994.76 Seconds
(without alignments)
9747.064 Million cell updates/sec

Title: US-09-788-074-2

Perfect score: 1279

Sequence: 1 aatggagcaacatctagc.....tctatgagaagtgcattga 1279

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	710.4	55.5	3260	3 BC053042	BC053042 Mus muscu
2	333	26.0	850	6 CB321549	CB321549 AGENCOURT
3	178.4	13.9	1501	6 CB590454	CB590454 AGENCOURT
4	178.2	13.9	658	1 AA435016	AA435016 ve06a06.r
5	176.6	13.8	293	6 BY791922	BY791922 BY791922
6	176.6	13.8	322	5 BY332071	BY332071 BY332071
7	176.6	13.8	326	5 BY331257	BY331257 BY331257
8	176.6	13.8	327	5 BY129217	BY129217 BY129217
9	176.6	13.8	327	5 BY141407	BY141407 BY141407
10	176.6	13.8	339	5 BY107737	BY107737 BY107737
11	176.6	13.8	341	6 BY784951	BY784951 BY784951
12	176.6	13.8	343	5 BY112490	BY112490 BY112490
13	176.6	13.8	347	5 BY112327	BY112327 BY112327
14	176.6	13.8	347	5 BY112363	BY112363 BY112363
15	176.6	13.8	352	5 BY340471	BY340471 BY340471
16	176.6	13.8	357	5 BY090269	BY090269 BY090269
17	176.6	13.8	358	6 BY768634	BY768634 BY768634
18	176.6	13.8	359	5 BY060959	BY060959 BY060959
19	176.6	13.8	363	5 BY088620	BY088620 BY088620
20	176.6	13.8	363	5 BY101057	BY101057 BY101057
21	176.6	13.8	366	5 BY089011	BY089011 BY089011
22	176.6	13.8	367	6 BY770777	BY770777 BY770777
23	176.6	13.8	374	5 BY320215	BY320215 BY320215
24	176.6	13.8	376	5 BY071168	BY071168 BY071168

25	176.6	13.8	377	5 BY072217	BY072217 BY072217
26	176.6	13.8	377	6 BY771110	BY771110 BY771110
27	176.6	13.8	381	5 BY086574	BY086574 BY086574
28	176.6	13.8	383	5 BY321403	BY321403 BY321403
29	176.6	13.8	394	5 BY094268	BY094268 BY094268
30	176.6	13.8	397	7 W16080	W16080 mb60h01.r1
31	176.6	13.8	399	5 BY083452	BY083452 BY083452
32	176.6	13.8	404	5 BY075831	BY075831 BY075831
33	176.6	13.8	418	5 BY062483	BY062483 BY062483
34	176.6	13.8	418	7 W09684	W09684 ma03h08.r1
35	176.6	13.8	421	5 BQ178050	BQ178050 UI-M-ERO-
36	176.6	13.8	455	1 AI194241	AI194241 us52f07.r
37	176.6	13.8	484	2 BE335677	BE335677 us87h12.y
38	176.6	13.8	505	5 BQ129927	BQ129927 i132h08.y
39	176.6	13.8	507	1 AA574742	AA574742 vm27a03.r
40	176.6	13.8	513	2 BE335596	BE335596 us87a09.y
41	176.6	13.8	519	1 AA271333	AA271333 vb78c11.r
42	176.6	13.8	527	1 AA647101	AA647101 vn39f11.x
43	176.6	13.8	542	4 BM729863	BM729863 lh83d12.y
44	176.6	13.8	546	7 W97909	W97909 mg05f07.r1
45	176.6	13.8	563	1 AA268290	AA268290 va40f12.x

ALIGNMENTS

RESULT 1	BC053042	3260 bp	mRNA	linear	HTC 05-JUN-2003
LOCUS	Mus musculus cDNA clone IMAGE:5687273, with apparent retained intron.				
DEFINITION	BC053042				
ACCESSION	BC053042				
VERSION	BC053042.1	GI:31418541			
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 3260)				
AUTHORS	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richard, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalieu, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3260)				
AUTHORS	Straussberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabbs-r@mail.nih.gov Tissue Procurement: Dr. Jim Lin, University of Iowa				


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Db      229  TTTGTAACCTGGGAGAGAGTTTGTATGAACGACAGCTGATGGCGAAGAACTGAGTCTAG 288
      310  CTACAAACATCTGTGAAGCGACAGAACTTCTAGATTTCAGATTAAATTCGATTAAACAA 369
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      370  TGTCTGTACTTACTCCAGGCGTGAAGTGAAGAACTTCTATGAGATTGACTTTTGTAT 429
      349  TGTCTGTACTTACTCCAGGCGTGAAGTGAAGAACTTCTATGAGATTGACTTTTGTAT 408
      430  AAATTAGTAAAGTCCAGGACTAAGAAATGAAGA 464
      409  AAATTAGTAAAGTCCAGGACTAAGAAATGAAGA 443

RESULT 3
CB590454      1501 bp      mRNA      linear      EST 03-APR-2003
LOCUS      AGENCOURT_12600409 NIH_MGC_136 Mus musculus cDNA clone
DEFINITION      IMAGE:30290371 5', mRNA sequence.
ACCESSION      CB590454
VERSION      CB590454
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 1501)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgapbs@mail.nih.gov
      Tissue Procurement: Dr. David Rowe
      cDNA Library Preparation: Invitrogen Corp
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
      DNA Sequencing by: Agencourt Bioscience Corporation
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LLNL at:
      http://image.llnl.gov
      Plate: NDAM330 row: o column: 20
      High quality sequence stop: 281.
      Location/Qualifiers
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      equivalents from respective days). Cloned directionally,
      oligo-dT primed (5'-GACTAGTCTAGATCGGCGCGCCCTGT)15-3'.
      Size selected for the >1kb fragments, average insert size
      1.2 kb. Normalization to Cot 7.5. Tissue contributed by
      David Rowe; library constructed by Resgen, Invitrogen
      Corp. Note: this is a NIH MGC Library."

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      Normalized, full-length enriched library from pool of
      mouse embryonic limb, maxilla and mandible, embryonic day
      17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw
      equivalents from respective days). Cloned directionally,
      oligo-dT primed (5'-GACTAGTCTAGATCGGCGCGCCCTGT)15-3'.
      Size selected for the >1kb fragments, average insert size
      1.2 kb. Normalization to Cot 7.5. Tissue contributed by
      David Rowe; library constructed by Resgen, Invitrogen
      Corp. Note: this is a NIH MGC Library."

ORIGIN
      Query Match      13.9%; Score 178.4; DB 6; Length 1501;
      Best Local Similarity 88.2%; Pred. No. 1.7e-39; Indels 0; Gaps 0;
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QY      130  AGGAGTAGGACTGGCTCTTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTTAC 189
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      190  GTGTGATGGCAACATCACCAGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249

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RESULT 4
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DEFINITION      5', similar to gb:X70100 rna2 M.musculus mall mRNA for keratinocyte
      lipid-binding (MOUSE);, mRNA sequence.
ACCESSION      AA435016
VERSION      AA435016
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 658)
AUTHORS      Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
      Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
      Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
      Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
      Watson, R.
TITLE      The WashU-HMI Mouse EST Project
JOURNAL      Unpublished (1996)
COMMENT      Contact: Marra M/Mouse EST Project
      WashU-HMI Mouse EST Project
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: mouseest@watson.wustl.edu
      This clone is available royalty-free through LLNL; contact the
      IMAGE Consortium (info@image.llnl.gov) for further information.
      Seq primer: -28mi3 rev2 ET from Amersham
      High quality sequence stop: 290.
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          /note="Vector: pT730-Pac (Pharmacia) with a modified
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      was primed with a Not I - oligo(dT) primer [5'
      TGTACCAATCTGAAGTGGAGCGCGCCGGAAGTTTTTTTTTTTTTTTTTTT
      3']; double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not
      I and Eco RI sites of the modified pT73 vector. RNA
      provided by Dr. Minoru Ko, Wayne State Univ. Library
      constructed and normalized by Bento Soares and M. Fatima
      Bonaldo."

FEATURES
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      polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
      was primed with a Not I - oligo(dT) primer [5'
      TGTACCAATCTGAAGTGGAGCGCGCCGGAAGTTTTTTTTTTTTTTTTTTT
      3']; double-stranded cDNA was ligated to Eco RI adaptors
      (Pharmacia), digested with Not I and cloned into the Not
      I and Eco RI sites of the modified pT73 vector. RNA
      provided by Dr. Minoru Ko, Wayne State Univ. Library
      constructed and normalized by Bento Soares and M. Fatima
      Bonaldo."

ORIGIN
      Query Match      13.9%; Score 178.2; DB 1; Length 658;
      Best Local Similarity 95.8%; Pred. No. 1.5e-39;
      Matches 183; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACTGTATCATTTAC 189
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RESULT 5
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 ACCESSION
 BY791922
 VERSION
 KEYWORDS
 SOURCE
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 293)
 REFERENCE
 AUTHORS
 Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M.,
 Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,
 Sugihara, Y., Saito, R., Osato, N., Nakamura, M., Shibata, Y., Yasunishi, A.,
 Hirozane-Kishikawa, T., Kusakabe, M., Gustincich, S., Beisel, K.,
 Kikuchi, N., Yoshiki, A., Nakagawa, A., Held, W. A., Iwata, H., Kono, T.,
 Pavan, W., Aidinis, V., Nakagawa, A., Hume, D. A., Fagiolini, M.,
 Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M.,
 Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,
 Muramatsu, M., Okazaki, Y., Kawai, J., and Hayashizaki, Y.
 Targeting a complex transcriptome: the construction of the mouse
 full-length cDNA encyclopedia
 Genome Res. 13 (6B), 1273-1289 (2003)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.jp/) for
 further details.

FEATURES
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 VERSION
 KEYWORDS
 SOURCE
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 322)
 REFERENCE
 AUTHORS
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
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 Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
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 Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
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 Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
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 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
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 whole body"

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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY141407 327 bp mRNA linear EST 09-DEC-2002
 BY141407 RIKEN full-length enriched, 17.5 days embryo whole body
 Mus musculus cDNA clone L930146D12 5', mRNA sequence.
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 ACCESSION
 VERSION
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 SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 327)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
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 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
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 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

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 12466851

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tgami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES
 Location/Qualifiers
 1..327

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 whole body"

ORIGIN

Query Match 13.8%; Score 176.6; DB 5; Length 327;
 Best Local Similarity 95.3%; Pred. No. 3.4e-39;
 Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 130 AGAGTAGAGCTGGCTCTTTAGGAAGTGGCTGCCATGGCCAGCCAGACTGTATCATTC 189

DB 128 AGAGTAGAGCTGGCTCTTTAGGAAGTGGCTGCCATGGCCAGCCAGACTGTATCATTC 187

QY 190 GTGTGATGTCACCAACATCACCTCAAAACCCAGACGACAGTGAACACCACTGTGTTCTC 249

DB 188 GTGTGATGTCACCAACATCACCTCAAAACCCAGACGACAGTGAACACCACTGTGTTCTC 247

QY 250 TTGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGGCAGAAAACTGAGTTCAG 309

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QY 310 CTACAAATAC 320

DB 308 CTGCACTTCC 318

RESULT 10
 BY107737

LOCUS
 DEFINITION
 Mus musculus cDNA clone L330014F16 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY107737 339 bp mRNA linear EST 07-DEC-2002
 Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 339)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
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Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Santalin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verdano, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

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Nature 420, 563-573 (2002)

22354683

12466851

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Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

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Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

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Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

Location/Qualifiers

1. .339

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="I330014F16"

/tissue_type="whole body"

/dev_stage="15 days embryo"

/clone_lib="RIKEN full-length enriched, 15 days embryo

whole body"

ORIGIN

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QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAGCCAGCCAGACTGTATCATTTAC 189

|||||

Db 99 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAGCCAGCCAGACTGTATCATTTAC 158

|||||

QY 190 GTGTGATGCGCAACATCACCGTCAAAACCGAGACGACAGTGAAGACGACTGTGTCTC 249

|||||

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|||||

QY 250 TTGTAACTGGGAGAGAAGTTTGATGAACACAGCTGATGGCAGAAAACTGAGTCAAG 309

|||||

Db 219 TTGTAACTGGGAGAGAAGTTTGATGAACACAGCTGATGGCAGAAAACTGAGACCGT 278

|||||

QY 310 CTACACATAC 320

|||||

Db 279 CTGCACCTTCC 289

|||||

RESULT 11

BY784951

LOCUS

DEFINITION

Mus musculus cDNA clone L930190A14 5', mRNA sequence.

ACCESSION

VERSION

BY784951.1

GI:39711590

EST

Mus musculus (house mouse)

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCES

1 (bases 1 to 341)

AUTHORS

Carninci, P., Waki, K., Shiraki, T., Konno, H., Shibata, K., Itoh, M.,

Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S.,

Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A.,

Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,

Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K.,

Pavan, W., Aidinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T.,

Nakauchi, H., Lyons, P., Wells, C., Hume, D. A., Fagioli, M.,

Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mombaerts, P.,

Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.

Targeting a complex transcriptome: the construction of the mouse

full-length cDNA encyclopedia

Genome Res. 13 (6B), 1273-1289 (2003)

22703353

12819125

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further details.

Location/Qualifiers

1. .341

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6J"

/db_xref="taxon:10090"

/clone="L930190A14"

/tissue_type="whole body"

/dev_stage="17.5 days embryo"

/clone_lib="RIKEN full-length enriched, 17.5 days embryo

whole body"

ORIGIN

Query Match

Best Local Similarity

Matches 182; Conservative

0; Mismatches 9; Indels

0; Gaps

QY

130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCAGCCAGCCAGACTGTATCATTTAC 189

|||||

Db 120 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACAGCTGTATCATTTAC 179
 QY 190 GTGTGATGGCAACAACATCACGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 249
 Db 180 GTGTGATGGCAACAACATCACGGTCAAAACCGAGAGCAGTGAAGACGACTGTGTCTC 239
 QY 250 TTGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGCCAGAAAACTGAGTCCAG 309
 Db 240 TTGTAACTGGGAGAGAGTTTGTATGAACGACAGCTGTATGCCAGAAAACTGAGACGGT 299
 QY 310 CTCAACATAC 320
 Db 300 CTGCACCTTCC 310

RESULT 12
 BY112490
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY112490 343 bp mRNA linear EST 07-DEC-2002
 BY112490 RIKEN full-length enriched, 18 days embryo whole body Mus
 musculus cDNA clone L430007B06 5', mRNA sequence.
 BY112490.1 GI:26223107
 EST.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE
 AUTHORS
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Iehii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354663
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
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FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
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 /clone="L430007B06"
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ORIGIN

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 Best Local Similarity 95.3%; Pred. No. 3.5e-39;
 Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAAAGCCAGACAGCTGTATCATTTAC 189
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 QY 310 CTCAACATAC 320
 Db 307 CTGCACCTTCC 317

RESULT 13

BY112327

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

REFERENCES

AUTHORS

REFERENCES

AUTHORS

REFERENCES

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/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L430005f10"
/tissue_type="whole body"
/dev_stage="18 days embryo"
/clone_lib="RIKEN full-length enriched, 18 days embryo whole body"

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|||||
QY 310 CTACAACATAC 320
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Db 311 CTGACACTTCC 321
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RESULT 14
LOCUS BY112363
DEFINITION BY112363 RIKEN full-length enriched, 18 days embryo whole body Mus musculus cDNA clone L430005M13 5', mRNA sequence.
ACCESSION BY112363
VERSION BY112363.1 GI:36222980
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 347)
AUTHORS
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, D., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@genome.gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, T., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers

source

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JOURNAL
MEDLINE
PUBMED
COMMENT

ORIGIN

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Best Local Similarity 95.3%; Pred. No. 3.5e-39;
Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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ACCESSION BY340471
VERSION BY340471.1 GI:26569959
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 352)
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuoka, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brucic, V., Chothia, C., Cousin, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Gusinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltsev, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomica, M., Verdano, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wu, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Waki, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
Location/Qualifiers
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ORIGIN

Query Match 13.8%; Score 176.6; DB 5; Length 352;
Best Local Similarity 95.3%; Pred. No. 3.5e-39;
Matches 182; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 130 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTAC 189
|||
Db 127 AGGAGTAGGACTGGCTCTTAGGAAGATGGCTGCCATGGCCAGCCAGACTGTATCATTAC 186
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QY 190 GTGTGATGGCAACAACATCACGGTCAAAACCGAGAGCACAGTGAAGACGACTGTGTTCTC 249
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Db 307 CTGCACCTTCC 317
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Search completed: July 12, 2005, 21:11:48
Job time : 4999.76 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	662	100.0	662	17	US-10-172-118-608
6	662	100.0	662	18	US-10-342-887-608
7	662	100.0	662	19	US-10-717-597-57

8	662	100.0	662	19	US-10-775-169-332	Sequence 332, App
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ALIGNMENTS

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US-09-788-074-4
; Sequence 4, Application US/09788074
; Patent No. US20010044110A1
; GENERAL INFORMATION:
; APPLICANT: Hotamisligil, Gokhan S.
; TITLE OF INVENTION: INHIBITION OF MAL1
; FILE REFERENCE: 21509-044
; CURRENT APPLICATION NUMBER: US/09/788,074
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,106
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 662
; TYPE: DNA
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RESULT 2

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; Sequence 95, Application US/10171581
; Publication No. US20030104426A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter
; APPLICANT: Mao Mao
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia
; FILE REFERENCE: 9301-157-999
; CURRENT APPLICATION NUMBER: US/10/171,581
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,914
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 366
; SEQ ID NO 95
; LENGTH: 662
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: M94856
; DATABASE ENTRY DATE: 2001-06-18
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; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsay, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22


```
QY 661 CT 662
Db 661 CT 662

RESULT 5
US-10-172-118-608
; Sequence 608, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 608
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 001444
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-608

Query Match 100.0%; Score 662; DB 17; Length 662;
Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGGCGAGCGAGACCCCTCTCTGACGCGCAGCCCGCGGACCCGACCCACCATGGCCACAGTT 60
Db 1 ACCGGCGAGCGAGACCCCTCTCTGACGCGCAGCCCGCGGACCCGACCCACCATGGCCACAGTT 60

QY 61 CAGCAGCTGGAAGGAGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 120
Db 61 CAGCAGCTGGAAGGAGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 120

QY 121 GAGCTAGGAGTGGGAATAGCTTTGGCAAAATTTGGCGCAATGGCGCAATGGCCAGCAGATTGTATC 180
Db 121 GAGCTAGGAGTGGGAATAGCTTTGGCAAAATTTGGCGCAATGGCGCAATGGCCAGCAGATTGTATC 180

QY 181 ATCACTTGTGATGTTAAACCTCACCATAAAATCTGAGAGCATTGTAAGAAACACACAG 240
Db 181 ATCACTTGTGATGTTAAACCTCACCATAAAATCTGAGAGCATTGTAAGAAACACACAG 240

QY 241 TTTTCTGTGATGTTAAAGGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 300
Db 241 TTTTCTGTGATGTTAAAGGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 300

QY 301 ACTGTCTGCAACTTTACAGATGGTGCATTGGTTGAGCAATCAGGAGTGGGATGGGAAGGAA 360
Db 301 ACTGTCTGCAACTTTACAGATGGTGCATTGGTTGAGCAATCAGGAGTGGGATGGGAAGGAA 360

QY 361 AGCACAATACAGAAATTTGAAGATGGGAATTTAGTGGTGGAGTGTCTATGACAAAT 420
Db 361 AGCACAATACAGAAATTTGAAGATGGGAATTTAGTGGTGGAGTGTCTATGACAAAT 420

QY 421 GTCACTGTACTCGGATCTATGAAAAGTAGAATAAAATTCATCATCTTGGACAG 480
Db 421 GTCACTGTACTCGGATCTATGAAAAGTAGAATAAAATTCATCATCTTGGACAG 480

QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540
Db 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTT 540

QY 661 CT 662
Db 661 CT 662

RESULT 6
US-10-342-887-608
; Sequence 608, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 608
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-608

Query Match 100.0%; Score 662; DB 18; Length 662;
Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCGGCGAGCGAGACCCCTCTCTGACGCGCAGCCCGCGGACCCGACCCACCATGGCCACAGTT 60
Db 1 ACCGGCGAGCGAGACCCCTCTCTGACGCGCAGCCCGCGGACCCGACCCACCATGGCCACAGTT 60

QY 61 CAGCAGCTGGAAGGAGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 120
Db 61 CAGCAGCTGGAAGGAGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 120

QY 121 GAGCTAGGAGTGGGAATAGCTTTGGCAAAATTTGGCGCAATGGCGCAATGGCCAGCAGATTGTATC 180
Db 121 GAGCTAGGAGTGGGAATAGCTTTGGCAAAATTTGGCGCAATGGCGCAATGGCCAGCAGATTGTATC 180

QY 181 ATCACTTGTGATGTTAAACCTCACCATAAAATCTGAGAGCATTGTAAGAAACACACAG 240
Db 181 ATCACTTGTGATGTTAAACCTCACCATAAAATCTGAGAGCATTGTAAGAAACACACAG 240

QY 241 TTTTCTGTGATGTTAAAGGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 300
Db 241 TTTTCTGTGATGTTAAAGGAGTGGCGCTGTGGACAGCAAGGCTTTGATGAATACATGAAG 300

QY 301 ACTGTCTGCAACTTTACAGATGGTGCATTGGTTGAGCAATCAGGAGTGGGATGGGAAGGAA 360
Db 301 ACTGTCTGCAACTTTACAGATGGTGCATTGGTTGAGCAATCAGGAGTGGGATGGGAAGGAA 360

QY 361 AGCACAATACAGAAATTTGAAGATGGGAATTTAGTGGTGGAGTGTCTATGACAAAT 420
Db 361 AGCACAATACAGAAATTTGAAGATGGGAATTTAGTGGTGGAGTGTCTATGACAAAT 420
```


Db 361 AGACACATACAGAGAAATGAAAGATGGAAATAGTGGTGGAGTGTGCATGACAAAT 420
QY 421 GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATCCATCATCACTTTGGACAG 480
Db 421 GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATCCATCATCACTTTGGACAG 480
QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCACTTTCTTT 540
Db 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCACTTTCTTT 540
QY 541 CTTTTTTTTTCAATCACTGTGTTCAATTAATCTTTATCATAAACATTTTACATGCGAGTAT 600
Db 541 CTTTTTTTTTCAATCACTGTGTTCAATTAATCTTTATCATAAACATTTTACATGCGAGTAT 600
QY 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
Db 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
QY 661 CT 662
Db 661 CT 662

RESULT 7

US-10-717-597-57
; Sequence 57, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dornier, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-57

Query Match 100.0%; Score 662; DB 19; Length 662;
Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGCGGACGACAGCCCTCTCTGACGCGCAGCCGCGCACCCACCATGCGCCACAGTT 60
Db 1 ACCGCGGACGACAGCCCTCTCTGACGCGCAGCCGCGCACCCACCATGCGCCACAGTT 60
QY 61 CAGCAGCTGGAAGGAAGATGGCGCTGTGGACAGCAAAAGGCTTTGATGAATACATGAAG 120
Db 61 CAGCAGCTGGAAGGAAGATGGCGCTGTGGACAGCAAAAGGCTTTGATGAATACATGAAG 120
QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAGATGATC 180
Db 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAGATGATC 180
QY 181 ATCACTTGTGATGGTAAAAACCTCACCATAAAAATCTGAGAGCAGCTTTGAAAAACAACAG 240
Db 181 ATCACTTGTGATGGTAAAAACCTCACCATAAAAATCTGAGAGCAGCTTTGAAAAACAACAG 240
QY 241 TTTTCTGTACCTCGGAGAGAAAGTTTGAAGAAACCAACAGCTGATGGCGAGAAAACTCAG 300

Db 241 TTTTCTGTACCTCGGAGAGAAAGTTTGAAGAAACCAACAGCTGATGGCAGAAAACTCAG 300
QY 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTACAGCATCAGGAGTGGATGGGAAGGAA 360
Db 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTACAGCATCAGGAGTGGATGGGAAGGAA 360
QY 361 AGCAACAATAACAAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCATGAACAAT 420
Db 361 AGCAACAATAACAAGAAATTTGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCATGAACAAT 420
QY 421 GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATCCATCATCACTTTGGACAG 480
Db 421 GTCACTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATCCATCATCACTTTGGACAG 480
QY 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCACTTTCTTT 540
Db 481 GAGTTAAATTAAGAGATGACCAAGCTCAGTTCATGAGCAAAATCTCCATCACTTTCTTT 540
QY 541 CTTTTTTTTTCAATCACTGTGTTCAATTAATCTTTATCATAAACATTTTACATGCGAGTAT 600
Db 541 CTTTTTTTTTCAATCACTGTGTTCAATTAATCTTTATCATAAACATTTTACATGCGAGTAT 600
QY 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
Db 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTTTGTG 660
QY 661 CT 662
Db 661 CT 662

RESULT 8

US-10-775-169-332
; Sequence 332, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 332
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-332

Query Match 100.0%; Score 662; DB 19; Length 662;
Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACCGCGGACGACAGCCCTCTCTGACGCGCAGCCGCGCACCCACCATGCGCCACAGTT 60
Db 1 ACCGCGGACGACAGCCCTCTCTGACGCGCAGCCGCGCACCCACCATGCGCCACAGTT 60
QY 61 CAGCAGCTGGAAGGAAGATGGCGCTGTGGACAGCAAAAGGCTTTGATGAATACATGAAG 120
Db 61 CAGCAGCTGGAAGGAAGATGGCGCTGTGGACAGCAAAAGGCTTTGATGAATACATGAAG 120
QY 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAGATGATC 180
Db 121 GAGCTAGGAGTGGGAATAGCTTTGCGAAAAATGGCGCAATGGCCAGATGATC 180
QY 181 ATCACTTGTGATGGTAAAAACCTCACCATAAAAATCTGAGAGCAGCTTTGAAAAACAACAG 240
Db 181 ATCACTTGTGATGGTAAAAACCTCACCATAAAAATCTGAGAGCAGCTTTGAAAAACAACAG 240

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QY 241 TTTTCTGTACCTGGGAGAGAGTTTGAAGAAACCAACAGCTGATGGGAGAGAAACTCAG 300
Db 241 TTTTCTGTACCTGGGAGAGAGTTTGAAGAAACCAACAGCTGATGGGAGAGAAACTCAG 300
QY 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTCAAGCATCAGGAGTGGGATGGGAGGAA 360
Db 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTCAAGCATCAGGAGTGGGATGGGAGGAA 360
QY 361 AGCAACAATAACAAGAAAAATTGAAGATGGGAAATTTAGTGGTGGAGTGTGCATGAACAAT 420
Db 361 AGCAACAATAACAAGAAAAATTGAAGATGGGAAATTTAGTGGTGGAGTGTGCATGAACAAT 420
QY 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAG 480
Db 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAG 480
QY 481 GAGTTAAATTGAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATACACTGTTTCTTT 540
Db 481 GAGTTAAATTGAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATACACTGTTTCTTT 540
QY 541 CTTTTTTTTTTCATTACTGTGTTCAATTATCTTTATCATATAAACAATTTTACATGCAGCTAT 600
Db 541 CTTTTTTTTTTCATTACTGTGTTCAATTATCTTTATCATATAAACAATTTTACATGCAGCTAT 600
QY 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAAATGTGTTTGTG 660
Db 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAAATGTGTTTGTG 660
QY 661 CT 662
Db 661 CT 662
```

RESULT 9

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US-10-788-792-24
; Sequence 24, Application US/10788792
; Publication No. US20040191819A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-792-24
```

```
Query Match 100.0%; Score 662; DB 19; Length 662;
Best Local Similarity 100.0%; Pred. No. 2.3e-162;
Matches 662; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ACCGCGGCGCAGACCCCTCTCTGCAGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCAGTT 60
Db 1 ACCGCGGCGCAGACCCCTCTCTGCAGCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCAGTT 60
QY 61 CAGCAGCTGGAAGGAGAGTGGGCGCTTGTGGAGCAGCAAAAGGCTTTGATGAATACATGAAG 120
Db 61 CAGCAGCTGGAAGGAGAGTGGGCGCTTGTGGAGCAGCAAAAGGCTTTGATGAATACATGAAG 120
QY 121 GAGCTAGGAGTGGGAATAGCTTTGGAAAAAATGGGCGCAATGGCCAGCCAGATTGTATC 180
Db 121 GAGCTAGGAGTGGGAATAGCTTTGGAAAAAATGGGCGCAATGGCCAGCCAGATTGTATC 180
QY 181 ATCAGTTGTGATGGTAAAAAACCTTACCATAAAAAATCTGAGAGCAGCTTTTGAAGAAACACACAG 240
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Db 181 ATCAGTTGTGATGGTAAAAAACCTTACCATAAAAAATCTGAGAGCAGCTTTTGAAGAAACACAG 240
QY 241 TTTTCTGTGACCTGGGAGAGAGTTTGAAGAAACCAACAGCTGATGGGAGAGAAACTCAG 300
Db 241 TTTTCTGTGACCTGGGAGAGAGTTTGAAGAAACCAACAGCTGATGGGAGAGAAACTCAG 300
QY 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTCAAGCATCAGGAGTGGGATGGGAGGAA 360
Db 301 ACTGCTGCAACTTTTACAGATGGTGCATTTGGTTTCAAGCATCAGGAGTGGGATGGGAGGAA 360
QY 361 AGCAACAATAACAAGAAAAATTGAAGATGGGAAATTTAGTGGTGGAGTGTGCATGAACAAT 420
Db 361 AGCAACAATAACAAGAAAAATTGAAGATGGGAAATTTAGTGGTGGAGTGTGCATGAACAAT 420
QY 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAG 480
Db 421 GTCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAG 480
QY 481 GAGTTAAATTGAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATACACTGTTTCTTT 540
Db 481 GAGTTAAATTGAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATACACTGTTTCTTT 540
QY 541 CTTTTTTTTTTCATTACTGTGTTCAATTATCTTTATCATATAAACAATTTTACATGCAGCTAT 600
Db 541 CTTTTTTTTTTCATTACTGTGTTCAATTATCTTTATCATATAAACAATTTTACATGCAGCTAT 600
QY 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAAATGTGTTTGTG 660
Db 601 TTCAAAGTGTGTGGATTAATAGGATCATCCCTTTGGTTAATAAATAAATGTGTTTGTG 660
QY 661 CT 662
Db 661 CT 662
```

RESULT 10

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US-09-971-392-113
; Sequence 113, Application US/09971392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Cecilia I.
; APPLICANT: Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 113
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Template ID: 995880.12
US-09-971-392-113
```

```
Query Match 99.7%; Score 660; DB 10; Length 1071;
Best Local Similarity 100.0%; Pred. No. 9.6e-162;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 3 CGCCGACGACAGACCCCTCTCTGCAGCGCCGCCGCCGCCGCCGCCGCCGCCGCCAGTTCA 62
Db 42 CGCCGACGACAGACCCCTCTCTGCAGCGCCGCCGCCGCCGCCGCCGCCGCCAGTTCA 101
QY 63 GCAGCTGGAAGGAGATGGCGCTTGTGGACGCAAGAGCTTTGATGATACATGAGCA 122
Db 102 GCAGCTGGAAGGAGATGGCGCTTGTGGACGCAAGAGCTTTGATGATACATGAGCA 161
```

QY 123 GCTAGAGTGGGAATAGCTTTTCGGAATAATGGCGCAATGGCCAGCCAGATTGTATCAT 182
DB 162 GCTAGAGTGGGAATAGCTTTTCGGAATAATGGCGCAATGGCCAGCCAGATTGTATCAT 221
QY 183 CACTTGTGATGTTAAACCACTCACCATAAATACTGAGAGCACTTTGAAAAACAACAGATT 242
DB 222 CACTTGTGATGTTAAACCACTCACCATAAATACTGAGAGCACTTTGAAAAACAACAGATT 281
QY 243 TTCTTGTACCCCTGGGAGAGAAGTTTGAAGAAACCAAGCTGATGGCAGAAAAAAGCTCAGAC 302
DB 282 TTCTTGTACCCCTGGGAGAGAAGTTTGAAGAAACCAAGCTGATGGCAGAAAAAAGCTCAGAC 341
QY 303 TGCTGCAACTTTACAGATGGTGCATTTGAGAAACCAAGCTGAGAGTGGGATGGGAAGAAAG 362
DB 342 TGCTGCAACTTTACAGATGGTGCATTTGAGAAACCAAGCTGAGAGTGGGATGGGAAGAAAG 401
QY 363 CACAATAACAGAAAAATGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCAATCAATGT 422
DB 402 CACAATAACAGAAAAATGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCAATCAATGT 461
QY 423 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAATAATTCATCATCACTTTGGACAGGA 482
DB 462 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAATAATTCATCATCACTTTGGACAGGA 521
QY 483 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAACTCCATCACTGTTCTTTCT 542
DB 522 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAACTCCATCACTGTTCTTTCT 581
QY 543 TTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATAAACATTTTACATGAGCTATTT 602
DB 582 TTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATAAACATTTTACATGAGCTATTT 641
QY 603 CAAAGTGTGTTGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTGTTGTGCT 662
DB 642 CAAAGTGTGTTGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTGTTGTGCT 701

RESULT 11

US-09-971-429B-52
; Sequence 52, Application US/09971429B
; Publication No. US20030175704A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K. W.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0040 US
; CURRENT APPLICATION NUMBER: US/09/971,429B
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/239,024
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PERL Program
; SEQ ID NO 52
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030175704A1 995880.12
US-09-971-429B-52

Query Match 99.7%; Score 660; DB 10; Length 1071;
Best Local Similarity 100.0%; Pred. No. 9.6e-162;
Matches 660; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 CGCCGACGACAGCCCTCTCTGACGCGCCGCGCCGACCCACCCATGCCACAGATTCA 62
DB 42 CGCCGACGACAGCCCTCTCTGACGCGCGCCGCGCCGACCCACCCATGCCACAGATTCA 101
QY 63 GCAGCTGGAAGGAAGATGGCGCTGTGTGACAGCAAGGCTTTGATGAATACATGAAGA 122
DB 102 GCAGCTGGAAGGAAGATGGCGCTGTGTGACAGCAAGGCTTTGATGAATACATGAAGA 161

QY 123 GCTAGAGTGGGAATAGCTTTTCGGAATAATGGCGCAATGGCCAGCCAGATTGTATCAT 182
DB 162 GCTAGAGTGGGAATAGCTTTTCGGAATAATGGCGCAATGGCCAGCCAGATTGTATCAT 221
QY 183 CACTTGTGATGTTAAACCACTCACCATAAATACTGAGAGCACTTTGAAAAACAACAGATT 242
DB 222 CACTTGTGATGTTAAACCACTCACCATAAATACTGAGAGCACTTTGAAAAACAACAGATT 281
QY 243 TTCTTGTACCCCTGGGAGAGAAGTTTGAAGAAACCAAGCTGATGGCAGAAAAAAGCTCAGAC 302
DB 282 TTCTTGTACCCCTGGGAGAGAAGTTTGAAGAAACCAAGCTGATGGCAGAAAAAAGCTCAGAC 341
QY 303 TGCTGCAACTTTACAGATGGTGCATTTGAGAAACCAAGCTGAGAGTGGGATGGGAAGAAAG 362
DB 342 TGCTGCAACTTTACAGATGGTGCATTTGAGAAACCAAGCTGAGAGTGGGATGGGAAGAAAG 401
QY 363 CACAATAACAGAAAAATGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCAATCAATGT 422
DB 402 CACAATAACAGAAAAATGAAAGATGGGAAATTTAGTGGTGGAGTGTGTCAATCAATGT 461
QY 423 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAATAATTCATCATCACTTTGGACAGGA 482
DB 462 CACCTGTACTCGGATCTATGAAAAAGTAGAATAAATAATTCATCATCACTTTGGACAGGA 521
QY 483 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAACTCCATCACTGTTCTTTCT 542
DB 522 GTTAATTAAGAGAATGACCAAGCTCAGTTCAATGAGCAAACTCCATCACTGTTCTTTCT 581
QY 543 TTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATAAACATTTTACATGAGCTATTT 602
DB 582 TTTTCTTTTTCATTACTGTGTTCAATTTATCTTTATCATAAACATTTTACATGAGCTATTT 641
QY 603 CAAAGTGTGTTGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTGTTGTGCT 662
DB 642 CAAAGTGTGTTGATTAATAGGATCATCCCTTTGGTTAATAAATAATGTGTTGTGCT 701

RESULT 12

US-10-240-965-143
; Sequence 143, Application US/10240965
; Publication No. US20030165924A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: SHIFFMAN, Dov
; APPLICANT: SOMOGYI, Roland
; APPLICANT: LAWN, Richard M.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: PORTER, Gordon J.
; APPLICANT: MIKITA, Thomas
; APPLICANT: TAI, Julie
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION
; FILE REFERENCE: PA-0025 PCT
; CURRENT APPLICATION NUMBER: US/10/240,965
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/195,106
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PERL Program
; SEQ ID NO 143
; LENGTH: 1072
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030165924A1 1099076.1
US-10-240-965-143

Query Match 98.0%; Score 649; DB 16; Length 1072;
Best Local Similarity 99.8%; Pred. No. 7.2e-159;
Matches 660; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 3 CGCCGACGACAGCCCTCTCTGACGCGCCGCGCCGACCCACCCAT-GGCCACAGTTC 61

42	CGCGACGACACCCCTCTCTGACGCCAGCCGCGCCAGCCACCATGGGCCACAGTTC	101
62	AGCAGCTGGAAGGAGATGCGCCCTGGTGACAGCAAAAGGCTTTGATGAATACATGAAGG	121
102	AGCAGCTGGAAGGAGATGCGCCCTGGTGGAAGCAAAAGGCTTTGATGAATACATGAAGG	161
122	AGCTAGGAGTGGGAATAGCTTTGCAAAAATGGGGCAATGGCCCAAGCCAGAGTTGTATCA	181
162	AGCTAGGAGTGGGAATAGCTTTGCAAAAATGGGGCAATGGCCCAAGCCAGAGTTGTATCA	221
182	TCACCTTGATGGTAAAAACCTTCACATAAAACTGAGAGCACTTTGAAAAACAACAGT	241
222	TCACCTTGATGGTAAAAACCTTCACATAAAACTGAGAGCACTTTGAAAAACAACAGT	281
242	TTTCTTGTAACCTGGGAGAGAAGTTTGAAGAAACCAACAGCTCATGGCGAAAAAATCTCAG	301
282	TTTCTTGTAACCTGGGAGAGAAGTTTGAAGAAACCAACAGCTCATGGCGAAAAAATCTCAG	341
302	CTGCTGCAACTTTACAGATGGTGTGATTTGAGTTCAGCATCAGGAGTGGGATGGGAAGGAA	361
342	CTGCTGCAACTTTACAGATGGTGTGATTTGAGTTCAGCATCAGGAGTGGGATGGGAAGGAA	401
362	GCACAAATCAAGAAAAATTGAAAGATGGGAATTAAGTGGTGGAGTGTGTCATGAACAATG	421
402	GCACAAATCAAGAAAAATTGAAAGATGGGAATTAAGTGGTGGAGTGTGTCATGAACAATG	461
422	TCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCACTTTGGACAGG	481
462	TCACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCACTTTGGACAGG	521
482	AGTTAATTAAGAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTTC	541
522	AGTTAATTAAGAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTTC	581
542	TTTTTTTTTTCATTAAGTGTGTTCAATATCTTTATCATAAAAATTTTACATGCAAGTATT	601
582	TTTTTTTTTTCATTAAGTGTGTTCAATATCTTTATCATAAAAATTTTACATGCAAGTATT	641
602	TCAAAGTGTGTTGGATTAATTAAGGATCATCCCTTTGGTTTAATAAATAAATGTTTGTGC	661
642	TCAAAGTGTGTTGGATTAATTAAGGATCATCCCTTTGGTTTAATAAATAAATGTTTGTGC	701
662	T 662	
702	T 702	

RESULT 13

US-09-920-455-23
; Sequence 23, Application US/09920455
; Patent No. US20020168647A1

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF HEAD AND NECK CANCER

;; TITLE OF INVENTION: AND D.
;; FILE REFERENCE: 210121.540

CURRENT APPLICATION NUMBER: US/09/920,455

; CURRENT FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 275

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; SOFTWARE: FastSEQ for Windows Version 4.0

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; SEQ ID NO 23
: LENGTH: 615
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; LENGTH: 615
; TYPE: DNA

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; LIFE: DNA
; ORGANISM:

FEATURE:

NAME/KEY

; LOCATION: 528, 553, 579

; OTHER INFORMATION: n = A,T,C
478 00 000 455 33

US-09-920-455-23

Query Match 89.1%: Score 590: DB 9: Length 615:

	Best Local Similarity	99.3%;	Pred. No. 1.4e-143;		Gaps	0; Indels	0; Mismatches	4; Matches	590; Conservative	
Qy	3	C G C G A G C G A G A C C C T C T C T G C A C G C C A G C C C G C G C A C C C A C C A T G G C C A C A G T T C A	62							
D b	22	C G C G A G C G A G A C C C C T C T C T G C A C G C C A G C C C G C G C A C C C A C C A T G G C C A C A G T T C A	81							
Qy	63	G C A G C T G S A A G A A G A T A G G C C T G T G G A C A G A A A G C T T T G A T A A T A C A T A G A A G G A	122							
D b	82	G C A G C T G S A A G A A G A T A G G C C T G T G G A C A G A A A G C T T T G A T A A T A C A T A G A A G G A	141							
Qy	123	G C T A G A G A T G G G A A T A G C T T T G C A A A A A T G G G C G C A A T G G C C A A G C C A G A T T G T A T C A T	182							
D b	142	G C T A G A G A T G G G A A T A G C T T T G C A A A A A T G G G C G C A A T G G C C A A G C C A G A T T G T A T C A T	201							
Qy	183	A C T T T G T A G T G T A A A A A C C T C A C C A T A A A A A C T G A G A G A C A C T T T G A A A A C A A C A G A T T	242							
D b	202	A C A T T T G T A G T G T A A A A A C C T C A C C A T A A A A A C T G A G A G A C A C T T T G A A A A C A A C A G A T T	261							
Qy	243	T T C T T G T P A C C C T C G G A G A G A A G T T T G A A G A A A C C A C A G C T G A T G G C A G A A A A A C T C A G A C	302							
D b	262	T T C T T G T A C C C T C G G A G A G A A G T T T G A A G A A A C C A C A G C T E A T G G C A G A A A A A C T C A G A C	321							
Qy	303	T G T C T G C A A C T T T A C A G A T G G T G C A T T G G F T T C A G C A T C A G A G T G G G A T G G G A A G A A G	362							
D b	322	T G T C T G C A A C T T T A C A G A T G G T G C A T T G G T T C A G C A T C A G A G T G G G A T G G G A A G A A G	381							
Qy	363	C A C A A T A C A G A A A A T T G A A G A T G G G A A A T T A G T G G T G G A G T G T C A T G A A C A A T G T	422							
D b	382	C A C A A T A C A G A A A A T T G A A G A T G G G A A A T T A G T G G T G G A G T G T C A T G A A C A A T G T	441							
Qy	423	C A C C T G T A C T C G G A T C T A T G A A A A A G T A G A A T A A A A A T T C C A T C A T C A C T T T T G G A C A G G A	482							
D b	442	C A C C T G T A C T C G G A T C T A T G A A A A A G T A G A A T A A A A A T T C C A T C A T C A C T T T T G G A C A G G A	501							
Qy	483	G T T A A T T A G A G A A T G N C A A G C A G T C A G T T C A A T G A C C A A T C T C C A T A C T G T T C T T T C T	542							
D b	502	G T T A A T T A G A G A A T G A C C A A G C T C A A T T C A A T G A C C A A A T C T C C A T A C T G T T C T T C T	561							
Qy	543	T T T T T T T T C A T T A C T G T G T T C A A T T A C T A T C T T T A T C A T A A A C A T T T T A C A T G C A G	596							
D b	562	T T T T T T T T C A T T A C T G N G N T C A A T T A C T T T A T C A T A A A C A T T T T A C A T G C A G	615							

RESULT 14

US-09-920-455-147

; Sequence 147, Application US/09920455

; Patent No. US20020168647A1

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

APPLICANT: Fan, Lique

;
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC
: TITLE OF INVENTION: AND DIAGNOSIS OF HEAD AND NECK CANCER

; TITLE OF INVENTION: AND DIAGNOSIS OF AIDS AND AIDS RELATED DISEASES
; FILE REFERENCE: 210121.540

1. THE APPLICANT'S CURRENT APPLICATION NUMBER

; CURRENT FILING DATE: 2001-08-01

; NUMBER OF SEQ ID NOS: 275

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; SOFTWARE: FastSEQ for Windows Version 4.0
CTC IN NO 147

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; SEQ ID NO 147
; LENGTH: 606

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LENGTH: 606
TYPE: DNA

; LIFE: DNA
; ORGANISM: H

FEATURE:

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; NAME/KEY: misc_feature
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; LOCATION

; OTHER INFORMATION: n = 155 147

US-09-920-455-147

Query Match 88.1% : Sco

Query Match
Best Local Simi

QV	6	CGACGCGAGACCCCTCTCTGCAAGCCAGCCGCGCCCGCACCCACCATGGCCACAGTTACGCA	65
Matches	583	Conservative	0; Mismatches 2; Indels 0; Gaps 0

Db	22	CGAGCAGACCCCTCTCTGACGCACGCCGCCGCCGCCACCCACCATGGCCACACAGTTTCAGCA	81
Qy	66	GCTGGAAGGAAGATGGCGCTCTGGTGGACAGCAAAAGCTTTGATGAATACATCAAGAGAGCT	125
Db	82	GCTGGAAGGAAGATGGCGCTCTGGTGGACAGCAAAAGCTTTGATGAATACATCAAGAGAGCT	141
Qy	126	AGGAGTGGGAATAGCTTTTCGCAAAAATGGCGCCATGGCCCAAGCCAGATTGTATCATCAC	185
Db	142	AGGAGTGGGAATAGCTTTTCGCAAAAATGGCGCCAAATGGCCCAAGCCAGATTGTATCATCAC	201
Qy	186	TTGTGATGCTAAAAACCTCACCATAAAAACTCAGAGACACTTTTGAAACCAACACAGTTTTC	245
Db	202	TTGTGATGGTAAAAACCTCACCATAAAAACTCAGAGACACTTTTGAAACCAACACAGTTTTC	261
Qy	246	TTGTACCTCGGAGAGAAGTTTGAAGAAACCAACAGCTGATGCGAGAAAACTCAGACTGT	305
Db	262	TTGTACCTCGGAGAGAAGTTTGAAGAAACCAACAGCTGATGCGAGAAAACTCAGACTGT	321
Qy	306	CTGCAACTTACAGATGTCGATCTGGTTCAGCATCAGAGTGGGATGGCAAGGAAGCAC	365
Db	322	CTGCAACTTACAGATGTCGATCTGGTTCAGCATCAGAGTGGGATGGCAAGGAAGCAC	381
Qy	366	AATAACAGAAAAATTGAAGAGATGGGAAATTAGTGGTGGAGTGTGTCATGAAACAAATGTCAC	425
Db	382	AATAACAGAAAAATTGAAGAGATGGGAAATTAGTGGTGGAGTGTGTCATGAAACAAATGTCAC	441
Qy	426	CTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAGAGTT	485
Db	442	CTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAGAGTT	501
Qy	486	AATTAAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCCCATACTGTTCTCTTTT	545
Db	502	AATTAAAGAGAATGACCAAGCTCAGTTCAATGAGCAAAATCCCATACTGTTCTCTTTT	561
Qy	546	TTTTTTCATTACTGTGTTCAATTATCTTTTATCATAAACATTTTAC	590
Db	562	TTTTTTCATTACTGTGTTCAATTATCTTTTATCATAAACATTTTAC	606

RESULT 15

US-09-981-151A-17

; Sequence 17, Application US/09981151A

; Publication No. US20030212256A1

; GENERAL INFORMATION:

; APPLICANT: Edinger, Shlomit R

; APPLICANT: Gerlach, Valerie

; APPLICANT: MacDougall, John R

; APPLICANT: Malyankar, Muriel M

; APPLICANT: Smithson, Glenda

; APPLICANT: Millet, Isabelle

; APPLICANT: Peyman, John A

; APPLICANT: Stone, David J

; APPLICANT: Gunther, Erik

; APPLICANT: Ellerman, Karen

; APPLICANT: Shimkets, Richard A

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Guo, Xiaojia

; APPLICANT: Patturajan, Meera

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Burgess, Catherine E

; APPLICANT: Zernusen, Bryan D

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Gangolli, Esha A

; APPLICANT: Fernandes, Elma R

; APPLICANT: Gorman, Linda

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-168

; CURRENT APPLICATION NUMBER: US/09/981,151A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 60/241,040

; PRIOR FILING DATE: 2000-10-17

/	PRIOR APPLICATION NUMBER:	60/241,058
/	PRIOR FILING DATE:	2000-10-17
/	PRIOR APPLICATION NUMBER:	60/241,063
/	PRIOR FILING DATE:	2000-10-17
/	PRIOR APPLICATION NUMBER:	60/241,243
/	PRIOR FILING DATE:	2000-10-17
/	PRIOR APPLICATION NUMBER:	60/242,152
/	PRIOR FILING DATE:	2000-10-20
/	PRIOR APPLICATION NUMBER:	60/242,482
/	PRIOR FILING DATE:	2000-10-23
/	PRIOR APPLICATION NUMBER:	60/242,611
/	PRIOR FILING DATE:	2000-10-23
/	PRIOR APPLICATION NUMBER:	60/242,612
/	PRIOR FILING DATE:	2000-10-23
/	PRIOR APPLICATION NUMBER:	60/242,880
/	PRIOR FILING DATE:	2000-10-24
/	PRIOR APPLICATION NUMBER:	60/242,881
/	PRIOR FILING DATE:	2000-10-24
/	Remaining Prior Application data removed - See File Wrapper or PALM.	
/	NUMBER OF SEQ ID NOS:	160
/	SOFTWARE:	PatentIn Ver. 2.1
/	SEQ ID NO 17	
/	LENGTH:	634
/	TYPE:	DNA
/	ORGANISM:	Homo sapiens
/	US-09-981-151A-17	
Query Match 80.9% Score 535.6; DB 10; Length 634;		
Best Local Similarity 92.6%; Prod.No. 2.3e-129; Indels 13; Gaps 2;		
Matches 589; Conservative 0; Mismatches 34;		
Qy	3	CGCGCAGCGACGACCCTCTCTGCACGCCAGCCCGCCGGCACCCACCATGGCCACAGTTCA 62
Db	12	CGCGCAGCGCAACCTCTGTCTGTATGCCCGCCCGCCGTCGCCACCATGGCCACAGTTCA 71
Qy	63	GCAAGTGGAAAGGAAGATGGCGCTGTGTGGACAGCAAAGCGCTTTTGATGAATACATGAAGGA 122
Db	72	GCAAGTGGGAGGAAGATGGCGCTGTGTGGACAGCAAACGCTTTTGATGAATACATGAAGGA 131
Qy	123	GCTTAGGAGTGGGAATAGCTTTTGGAAAAATGGCGGCAATGGCCCAAGCCAGATTGTATCAT 182
Db	132	GGGAGAGTGGGAATAGCTTTTGGAAAAATGGGACGCAATGGCCCAAGCCAGATTGTATCAT 191
Qy	183	CACCTTGTGATGGTAAAAAACCTCCACCATAAAAACTGAGAGCACCTTTGAAAACAACACAGTT 242
Db	192	CACCTTGTGATGGCAAAAACTTACCATAAAAAACCGAGAGCACCTTTGNA---AACACAGTT 248
Qy	243	TTCCTGTACCCCTGGGAGAGAAGTTTGAAGAAACCAAGCTGATGGCAGAAAAACTCAGAC 302
Db	249	TTCCTGTACCCCTGGGAGAGAAGTTTGAAGAAACCAAGCTGATGGCAGAAAAACTCAGAC 308
Qy	303	TGCTCCGACCTTTACAGATGGTGCATTTGTTTCAGCATCAGGAGTGGATGGGAAGGAAAG 362
Db	309	TGTTGTGAGCTTTTGCAGATGGTGCATTTGTTTCAGCATCAGGAGTGGATGGGAAGGAAAG 368
Qy	363	CACAATAACAAGAAAAATGAAAGATGGGAAAATAGTGGTGGAGTGTGT CATGAACAATGT 422
Db	369	CACAATAACAAGAAAAATGAAAGATGGGAAAATAGTGGTGTGTGT CATGAACAATGT 428
Qy	423	CACCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAGGA 482
Db	429	CGCCTGTACTCGGATCTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAGGA 488
Qy	483	GTTTAATTAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCAATCTGTTCTTCT 542
Db	489	GTTTAATTAAGAAATGACCAAGCTCAGTTCAATGAGCAAAATCTCCAATCTGTTCTTCT 539
Qy	543	TTTTTTTTTTCATTACTGTGTTCAAATTTATCTTTATCATATAAACATTTTTACATGCAGTATTT 602
Db	540	-TTTTTTTTTTCATTACTGTGTTCAAATTTATCTTTATCATATAAACATTTTTACATGCAGTATTT 598
Qy	603	CAAAGTGTGTGGATTAATTTAGGATCATCCCTTTGG 638

Db 599 CAAAGTGTCTTGGATTAAATTAGGATCATCCCTTTGG 634

Search completed: July 12, 2005, 19:05:22
Job time : 1170.11 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 12, 2005, 15:11:38 ; Search time 130.285 Seconds
(without alignments)
8314.170 Million cell updates/sec

Title: US-09-788-074-4
Perfect score: 662
Sequence: 1 accgcgcagcagaccctc.....taataataatgtttgtgtgt 662

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/ina/6B COMB.seq: *
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6: /cgn2_6/prodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	645	97.4	45762	4	US-09-949-016-16651
2	408	61.6	408	1	US-08-446-600A-3
3	350	52.9	354	3	US-09-643-597-143
4	350	52.9	354	4	US-09-480-884A-143
5	350	52.9	354	4	US-09-542-615A-143
6	350	52.9	354	4	US-09-606-421B-143
7	350	52.9	354	4	US-09-221-107-143
8	350	52.9	354	4	US-09-466-396A-143
9	350	52.9	354	4	US-09-476-496A-143
10	350	52.9	354	4	US-09-630-940B-143
11	350	52.9	354	4	US-09-285-479-143
12	155.8	23.5	620	4	US-09-949-016-1540
13	149.6	22.6	2150	4	US-09-949-016-389
14	148	22.4	2149	4	US-09-949-016-1539
15	143.4	21.7	463	4	US-09-513-999C-14348
16	137.6	20.8	429	4	US-09-799-451-387
17	128.2	19.4	267	4	US-09-513-999C-893
18	120.4	18.2	731	3	US-09-043-646-1
19	120.4	18.2	731	4	US-09-971-187-1
20	120.4	18.2	1022	4	US-09-949-016-1203
21	115	17.4	606	4	US-09-513-999C-3961
22	113.2	17.1	493	4	US-09-513-999C-3851
23	84.4	12.7	611	4	US-09-621-976-12879
24	74	11.2	8524	4	US-09-949-016-13282
25	73.6	11.1	9739	4	US-09-949-016-12131
26	73.6	11.1	9739	4	US-09-949-016-13281
27	63	9.5	286	4	US-09-513-999C-1409

C 28	62.2	9.4	7218	1	US-08-232-463-14	Sequence 14, Appl
29	60.8	9.2	601	4	US-09-949-016-42044	Sequence 42044, A
30	60.8	9.2	8597	4	US-09-949-016-12945	Sequence 12945, A
31	55.6	8.4	276	4	US-09-471-276-676	Sequence 676, App
32	49	7.4	405	4	US-09-949-016-5760	Sequence 5760, App
33	49	7.4	1287	4	US-09-774-528-249	Sequence 249, App
34	47.2	7.1	354	4	US-09-513-999C-1607	Sequence 1607, App
35	47	7.1	458	4	US-09-621-976-17115	Sequence 17115, A
36	44	6.6	640	2	US-08-847-724-2	Sequence 2, Appl
37	43.8	6.6	466	4	US-09-702-705-61	Sequence 61, Appl
38	43.8	6.6	466	4	US-09-736-457-61	Sequence 61, Appl
39	43.8	6.6	466	4	US-09-614-124B-61	Sequence 61, Appl
40	43.8	6.6	466	4	US-09-671-325-61	Sequence 61, Appl
41	43.8	6.6	466	4	US-09-589-184-61	Sequence 61, Appl
42	43.8	6.6	466	4	US-09-658-824-61	Sequence 61, Appl
43	43.8	6.6	924	1	US-08-468-709B-1	Sequence 1, Appl
44	43.8	6.6	924	2	US-08-241-664B-1	Sequence 1, Appl
45	43.8	6.6	924	4	US-09-640-173-174	Sequence 174, App

ALIGNMENTS

RESULT 1
US-09-949-016-16651/c
; Sequence 16651, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16651
; LENGTH: 45762
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16651

Query Match 97.4%; Score 645; DB 4; Length 45762;
Best Local Similarity 100.0%; Pred. No. 1.2e-178;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	18	CTCTCTGCACGCCAGCCCGCCGACCAATGATGAATACATCAAGAGCTAGGAGTGGGAAT	77
Db	28146	CTCTCTGCACGCCAGCCCGCCGACCAATGATGAATACATCAAGAGCTAGGAGTGGGAAT	28087
QY	78	ATGGCGCCCTGGTGGAGCAGCAAGGCTTTCATGAATACATCAAGAGCTAGGAGTGGGAAT	137
Db	28086	ATGGCGCCCTGGTGGAGCAGCAAGGCTTTCATGAATACATCAAGAGCTAGGAGTGGGAAT	28027
QY	138	AGCTTTGCCAAAATATGGGCGCAATGGCCAAAGCCAGATTTATCATCTGTGATGTAA	197
Db	28026	AGCTTTGCCAAAATATGGGCGCAATGGCCAAAGCCAGATTTATCATCTGTGATGTAA	27967
QY	198	AAACCTCACCATAAACTGAGAGCACTTTGAAAACAACACAGTTTTCTGTACCTGGG	257
Db	27966	AAACCTCACCATAAACTGAGAGCACTTTGAAAACAACACAGTTTTCTGTACCTGGG	27907
QY	258	AGAGAAGTTTGAAGAAACACACAGCTGATGGCGAAAAAATCTCAGACTGTCTGCAACTTTAC	317
Db	27906	AGAGAAGTTTGAAGAAACACACAGCTGATGGCGAAAAAATCTCAGACTGTCTGCAACTTTAC	27847
QY	318	AGATGGTGCATTGGTTTCAGCATCAGGATGGGATGGGAAGGAAAGCAATAACAGAAA	377

Db 27846 AGATGGTGCATGGTTTCAGCATCAGAGTGGAGTGGAGGAGGAGCAATTAACAGAGAA 27787
Qy 378 ATTGAAGATGGGAATTTAGTGGTGGAGTGTGTCAATGAACAATGTCACTGTACTCGGAT 437
Db 27786 ATTGAAGATGGGAATTTAGTGGTGGAGTGTGTCAATGAACAATGTCACTGTACTCGGAT 27727
Qy 438 CTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAGGAGTTAATTAAGAGAA 497
Db 27726 CTATGAAAAAGTAGAATAAAAAATTCATCATCATCTTTGGACAGGAGTTAATTAAGAGAA 27667
Qy 498 GACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTCTTTTTCATTAC 557
Db 27666 GACCAAGCTCAGTTCAATGAGCAAAATCTCCATCTGTTTCTTCTTTTTCATTAC 27607
Qy 558 TGTGTTCAATATCTTTATCATATAAATTTTACATGCAGCTATTTCAAAGTGTGTGAT 617
Db 27606 TGTGTTCAATATCTTTATCATATAAATTTTACATGCAGCTATTTCAAAGTGTGTGAT 27547
Qy 618 TAAATTAGATCATCCCTTTGGTTAATAAATAAATGTGTTGCT 662
Db 27546 TAAATTAGATCATCCCTTTGGTTAATAAATAAATGTGTTGCT 27502

RESULT 2
US-08-446-600A-3
; Sequence 3, Application US/08446600A
; Patent No. 5719126
; GENERAL INFORMATION:
; APPLICANT: No. 5719126dlund, James J. and Paroqui, Jamal Z.
; TITLE OF INVENTION: MELANOGENIC INHIBITOR, AND METHODS OF PRODUCING AND USING THE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; STREET: 2500 PNC Center, 201 East Fifth St.
; CITY: Cincinnati
; STATE: OH
; COUNTRY: USA
; ZIP: 45202-4182

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,600A
; FILING DATE: 24 May 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/980,513
; FILING DATE: 24 No. 5719126ember 1992
; APPLICATION NUMBER: PCT/US93/11139
; FILING DATE: 16 No. 5719126ember 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann G. Robinson
; REGISTRATION NUMBER: 39,820
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (513) 651-6128
; TELEFAX: (513) 651-6981
; TELEX: 21-4396 F&J Cin
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 bases
; TYPE: nucleic acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
US-08-446-600A-3

Query Match 61.6%; Score 408; DB 1; Length 408;
Best Local Similarity 100.0%; Pred. No. 5.2e-110;
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 ATGCCACAGTTTCAGCAGCTGGAAGGAAGATGGCGCCCTGGTGGACAGCAAAAGGCTTTGAT 108
Db 1 ATGCCACAGTTTCAGCAGCTGGAAGGAAGATGGCGCCCTGGTGGACAGCAAAAGGCTTTGAT 60
Qy 109 GAATACATGAAGGAGCTAGGAGTGGGAATAGCTTTTGGAAAAATGGGCGCAATGGCCAAAG 168
Db 61 GAATACATGAAGGAGCTAGGAGTGGGAATAGCTTTTGGAAAAATGGGCGCAATGGCCAAAG 120
Qy 169 CCAGATTGTATCATCTTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACTTTG 228
Db 121 CCAGATTGTATCATCTTGTGATGGTAAAAACCTCACCATAAAAACTGAGAGCACTTTG 180
Qy 229 AAAACAACACAGTTTCTTTGTACCTGGGAGAGAAATTTGAAGAAACCAACAGCTGATGCG 288
Db 181 AAAACAACACAGTTTCTTTGTACCTGGGAGAGAAATTTGAAGAAACCAACAGCTGATGCG 240
Qy 289 AGAAAACTCAGACTGTCTGCACTTTTACAGATGGTGTGATTTGTTTCAAGATCAGAGTGG 348
Db 241 AGAAAACTCAGACTGTCTGCACTTTTACAGATGGTGTGATTTGTTTCAAGATCAGAGTGG 300
Qy 349 GATGGGAAGGAAGCAACATTAACAGAAATTTGAAGATGGGAATTTAGTGTGGAGTGT 408
Db 301 GATGGGAAGGAAGCAACATTAACAGAAATTTGAAGATGGGAATTTAGTGTGGAGTGT 360
Qy 409 GTCATGAACAATGTCACTGTCTGATCTATGAAAAAGTAGAATAA 456
Db 361 GTCATGAACAATGTCACTGTCTGATCTATGAAAAAGTAGAATAA 408

RESULT 3

US-09-643-597-143
; Sequence 143, Application US/09643597
; Patent No. 6426072

; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 143
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-143

Query Match 52.9%; Score 350; DB 3; Length 354;
Best Local Similarity 100.0%; Pred. No. 5.7e-93;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 CTGATGGCAGAAAAACTCAGACTGTCTGCAACTTTTACAGATGGTGCATTGGTTTCAGCATC 340
Db 5 CTGATGGCAGAAAAACTCAGACTGTCTGCAACTTTTACAGATGGTGCATTGGTTTCAGCATC 64
Qy 341 AGGAGTGGGATGGGAAGGAGGAGCAATAAACAAGAAAAATGGAAGATGGGAAATTTAGTGG 400
Db 65 AGGAGTGGGATGGGAAGGAGGAGCAATAAACAAGAAAAATGGAAGATGGGAAATTTAGTGG 124
Qy 401 TGGAGTGTGTCAATGAACAATGTCACTGTCTGATCTATGAAAAAGTAGAATAAAT 460
Db 125 TGGAGTGTGTCAATGAACAATGTCACTGTCTGATCTATGAAAAAGTAGAATAAAT 184

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1540
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1540

Query Match 23.5%; Score 155.8; DB 4; Length 620;
Best Local Similarity 62.4%; Pred. No. 1.2e-35;
Matches 244; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 68 TGAAGGAGGATGGCGCTGGTGGACAGCAAGGCTTTGATGAATACATGAAGGAGCTAG 127
DB 61 TTGTAGGTACCTGGAACTTGTCTCCAGTGAAACTTTTGTGATTTATATGAAGAGTAG 120

QY 128 GAGTGGGAATAGCTTTGGCAAAATGGGCGCAATGGCCAAAGCCAGATTTGTATCATCACTT 187
DB 121 GAGTGGGCTTTGCCACAGGAAGTGGCTGGCATGGCCAAACCTTAACATGATCATCACTG 180

QY 188 GTGATGGTAAACCTCACCATAAACTGAGAGCACATTTGAAACAACACAGTTTCTT 247
DB 181 TGAATGGGGGTGTGATCACCATAAATCTGAAAGTACCTTTTAAATACTGAGATTTCT 240

QY 248 GTACCTGGGAGAGAGTTTGAAGAAACACAGCTGATGGCGAGAAACTCAGACTGTCT 307
DB 241 TCATCTGGCCAGGAATTTGACGAAGTCACTGAGATGACAGGAAGTCAAGACCA 300

QY 308 GCAACTTTACAGATGGTGCATTGGTTACAGCATCAGAGTGGGATGGGAGGAAAGCAAA 367
DB 301 TAACTTAGATGGGGTGTCTGGTACATGTGCAGAAATGGGATGGAAATCAACCA 360

QY 368 TAAAGAAATTTGAAGATGGGAATTTAGTGGTGGAGTGTCTCATGAATGTCACTT 427
DB 361 TAAAGAGAAACGAGAGGATGATTAACCTGGTGGTGGAAATGGGTCAATGAAGCGTCACTT 420

QY 428 GTACTCGGATCTATCAAAAGTGAATAAAA 458
DB 421 CCACAGAGTTTATGAGAGCATTAAGCCAA 451

RESULT 13
US-09-949-016-389
; Sequence 389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-389

Query Match 22.6%; Score 149.6; DB 4; Length 2150;

Best Local Similarity 54.6%; Pred. No. 1.6e-33;
Matches 299; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 73 GGAAGATGGCGCTGGTGGACAGCAAGGCTTTGATGAATACATGAGGAGCTAGGAGTGTG 132
DB 53 GGCACCTGGAACTTGTCTCTGACGAGAACTTTGACGATTAACAGAAAGTCTCTGGGTGTG 112

QY 133 GGAATAGCTTTGGCAAAATGGCGCAATGGCCAAAGCCAGATTTGATCATCACTTTGTGAT 192
DB 113 GGGTTAGCCACAGAAACTTGGGAAATTTGGCCAAACCCACTGTGATCATCAGCAAGAA 172

QY 193 GGTAAAAACCTCACATAAAACTGAGAGCACTTTGAAAAACAACACAGATTTCTTTGTACC 252
DB 173 GGAGATATTATACTATACGAACCTGAAAGTACCTTTTAAAAATACAGAAATCTCTTTCAAG 232

QY 253 CTGGGAGAGAGTTTGAAGAAACCCAGCTGATGGCAGAAAACTCAGACTGTCTGCAAC 312
DB 233 CTAGGCCAGGAATTTGAAGAAACCCAGCTGATGAAGAAACCCAGAGCATCTGTAACC 292

QY 313 TTTCAGATGTGCTGCTGTTTTCAGCATCAGGAGTGGGATGGGAGGAAAGCACAATAACA 372
DB 293 CTGACAGAGATCACTGAATCAAGTGCAGAGATGGGATGGCAAGACCAACCAATAAG 352

QY 373 AGAAATTTGAAGATGGGAAATTTAGTGGTGGAGTGTGTCATGAAACAATGTCTGTA 432
DB 353 AGAAAGCTAGTGAATGGGAAATTTAGTGGGAAATTTGAAGGCGGTGGTGTGCACC 412

QY 433 CGGATCTATGAAGATGAGATAAAATTCATCATCACTTTGGCAGAGGATTAATAAG 492
DB 413 AGAATCTATGAGAGGCTGGAATAATTCATTTCAATGGAAGTGGCTTTTATCAATTA 472

QY 493 AGAATGACCAAGCTCAGTTCAATGAGCAAACTCTCCATACTGTTCTTTCTTTTTC 552
DB 473 TGATGGAATCAATGCTTCCATTGCAAAAATGATGATCACTGCAAAATTTGTTTTC 532

QY 553 ATTACTGTGTTCAATTAATTTTATCAATAAAATTTTACATGAGCTATTTCAAAGTGTGT 612
DB 533 TTTTGTCTTAATATATCATGATATGCAAGGCTTAAACTGAGAAATTAATCTAAAGTCAGT 592

QY 613 TGGATTA 620
DB 593 GTTATTTA 600

RESULT 14
US-09-949-016-1539
; Sequence 1539, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1539
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1539

Query Match 22.4%; Score 148; DB 4; Length 2149;
Best Local Similarity 54.4%; Pred. No. 4.6e-33;
Matches 298; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

QY 73 GGAAGATGGCGCTGGTGGACAGCAAAAGGCTTTGATGATATACATGAAGAGCTAGAGTG 132
Db 53 GGCACCTGGAAACTTGTCTCTAGTGAGAACTTTGACGATTTACATGAAGCTCTGGGTGTG 112
QY 133 GGAATAGCTTTGGGAAAAATGGCGCAATGGCCCAAGCCAGATTGTATCATCACTTTGTGAT 192
Db 113 GGGTTAGCCACCGAATACTGGGAAATTTGGCCAAACCCACTGTGATCATCAGCAAGAA 172
QY 193 GGTAAAACTCCACCATAAAACTGAGAGCACTTTTGAAAAACAACACAGTTTCTTGATCC 252
Db 173 GGAATATTATTAATACGAACTGAAAGTACCTTTAAAAATACAGAAATCTCTTCAAG 232
QY 253 CTGGGAGAGAGTTTGAAGAAACCAAGCTGATGGCAGAAAAAATCACTGAGCTGTCTGCAAC 312
Db 233 CTAGGCCAGGAATTTGAAGAAACCAAGCTGCAATAGAAAGCAAGAGCATCGTAACC 292
QY 313 TTTACAGATGGTCAATGGTTTCAGCATCAGGAGTGGGATGGGAAGCAAAAGCAATAACA 372
Db 293 CTGCAGAGAGTCACTGAATCAAGTCAGAGATGGGATGGGCAAGAGCAACCATTAAG 352
QY 373 AGAAAAATTGAAAGATGGGAAATTTAGTGGTGGAGTGTCTCATGAACAATGTCACCTGTACT 432
Db 353 AGAAGCTAGTGAATGGGAAATTTAGTGGGATGTAATGAAGGCGTGGTGTGCACC 412
QY 433 CGGATCTGTGAAAAAGTAGAATAAAATTTCCATCATCACTTTGGCAGAGAGTTAATTAAG 492
Db 413 AGAATCTATGAGAAGCTTGAATAATCAATTTCTTCAATGAAAGTGGCTTTTATCATTTAA 472
QY 493 AGAATCAACCAAGCTCAGTTCAATGAGCAAAATCCATCTCTTTCTTTTCTTTTCTTTC 552
Db 473 TGATGGAATCAATGCTTCCATGTGACAAACTGAATACACTGCAAAATTTGTTTTTGC 532
QY 553 ATTACTGTGTTCAATATCTTTATCATATAACAATTTTACATGCAGCTATTTCAAAGTGTG 612
Db 533 TTTTGTCTTAATATATACAGATATGCAAGGCCCTAAACTGAGAAATTAATCTAAAGTCACT 592
QY 613 TGAATTA 620
Db 593 GTTATTTA 600

RESULT 15

US-09-513-999C-14348
; Sequence 14348, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14348
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 289
; OTHER INFORMATION: y=c or t
US-09-513-999C-14348

Query Match 21.7%; Score 143.4; DB 4; Length 463;
Best Local Similarity 62.4%; Pred. No. 4.4e-32;
Matches 239; Conservative 1; Mismatches 142; Indels 1; Gaps 1;
QY 68 TGAAGGAAGATGGCGCTGGTGGACAGCAAAAGGCTTTGATGAATACATGAAGAGCTAG 127

Db 82 TTGTAGGTACCTGGAAACTTTGCTCCAGTGAATACTTTGATGATTATATGAAGAAGTAG 141
QY 128 GAGTGGGAATAGCTTTTGGAAAAATGGGCGCAATGGCCCAAGCCAGATTGTATCATCACTT 187
Db 142 GAGTGGGCTTTGGCCACCAGGAAGTGGCTGGCATGGCCAAACCTTAACATGATCATCAGTG 201
QY 188 GTGATGTAAAAACCTTCACATAAAACTGAGAGCACTTTGAAAAACAACACAGTTTCTT 247
Db 202 TGAATGGGATGTGATCACCATTAAATCTGAAAAGTACCTTTAAAAATACTGAGATTTCCT 261
QY 248 GTACCTGGGAGAGAGTTTGAAGAAACCAAGCTGATGGCAGAAAACTCAGACTGTCT 307
Db 262 TCATACTGGGCCAGGAATTTGACG-AAGYACTGCAGATGACAGGAAGTCAAGAGCACCA 320
QY 308 GCAACTTTACAGATGGTGCATTTGGTTTCAGCATCAGGATGGGATGGGAAGCAAGCAAA 367
Db 321 TAACTTAGATGGGCTGCTGTTACATGTGCAGAAATGGGATGGGAATCAACCA 380
QY 368 TAACAAGAAAAATTGAAAGATGGGAATTTAGTGGTGGAGTGTGTCATGAACAATGTCACT 427
Db 381 TAAAGAGAAAAACGAGAGGATGATAAACTGGTGGTGAATGCGTGCATGAAAGCGTCACTT 440
QY 428 GTACTCGGATCTATGAAAGTA 450
Db 441 CCACGAGAGTTTATGAGAGCA 463

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